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OM protein - protein search, using sw model

Run on: December 1, 2004, 15:26:43 ; Search time 154 Seconds
(without alignments) 423.953 Million cell updates

Title: US-09-602-597A-4
Perfect score: 930
Sequence: 1 MAFFPSKVSTRTSSPAQAE.....QAWRGVGSNAATSQMAGGYA 182

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 segs. 358729299 residues

total number of hits satisfying chosen parameters: 2002273

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

```
Database :
A_Geneseq_23Sep04.*
1: Geneseqpl90s.*
2: Geneseqpl90s.*
3: Geneseqpl90s.*
4: Geneseqp2000s.*
5: Geneseqp2001s.*
6: Geneseqp2002s.*
7: Geneseqp2003as.*
8: Geneseqp2003bs.*
9: Geneseqp2004s.*
```

SUMMARIES

Result No.	Score	Query		Length	DB	ID	Description
		Match					
1	930	100.0	182	3	AAAY70458	Aay70458	Human mem
2	930	100.0	182	8	ADNO4054	Adn04054	Antipsori
3	930	100.0	182	8	AOS55157	Aos55157	Protein #
4	930	100.0	182	4	AAB61164	Aab61164	Human BBS
5	848	91.2	182	2	AA997999	Aa997999	NTII-11 n
6	625	67.2	125	5	ABBS0064	Abb90064	Human pol
7	580	62.4	113	3	AAB34711	Aab34711	Human sec
8	580	62.4	113	5	ABBS90110	Abs90110	Human pol
9	325	34.9	173	3	AAYS3643	Aays3643	A Bone ma
10	322	34.6	173	4	AAAM25799	Aam25799	Human pro
11	307	33.0	153	2	AAW52117	Aaw52117	Human pro
12	283	30.4	132	5	ABP41095	Abp41095	Human ova
13	205.5	22.2	527	4	ABG15862	Abg15862	Novel hum
14	191	20.5	100	6	ADA57177	Ada57177	Human sec
15	191	20.5	100	6	ADA41044	Ada41044	Human sec
16	191	20.5	100	6	ABR47899	AbR47899	Human sec
17	191	20.5	100	7	ADC74294	Adc74294	Human sec
18	191	20.5	101	2	AAAY41391	Aay41391	Human sec
19	183	17.4	145	4	AAO12388	Aao12388	Human pol
20	162	17.4	176	4	ABAB2597	Abab2597	Human tra
21	162	17.4	176	4	AAE03822	Aae03822	Human gen
22	162	17.4	176	5	ABP69675	Abp69675	Human pol
23	162	17.4	176	5	ABG96412	Abg96412	Human ova
24	162	17.4	176	5	ABG64565	Abg64565	Human alb
25	162	17.4	176	6	ABJ37034	Abj37034	Human bre

RESULT 1
AAY70458
TD AAY

AA
AC
AA70458:

21-JUN-2000 (first entry)

Human membrane channel protein-8 (MECHP-8).

Membrane channel protein-8; MECHP-8; diagnosis: treatment; lymphoma; cell proliferative disorder; buritis; atherosclerosis; cancer; sarcoma; inflammatory disorder; AIDS; Addison's disease; cystic fibrosis; asthma; diabetes mellitus; osmoregulatory disorder; diarrhoea; renal failure; muscular disorder; myocarditis; Duchenne's muscular dystrophy; nototropic; cardiovascular disorder; hypertension; bronchitis; vasculitis; cardiac; neurological disorder; Alzheimer's disease; Parkinson's disease; human; Huntington's disease; antiarteriosclerotic; hepatotropic; cytostatic; anti-HIV; antiamebic; neuroprotective; immunomodulator; antidiabetic; hypoglycemic; vasotropic; antisthmatic; antiinflammatory; antidepressant; antihypertensive; antiparkinsonian; immunostimulant.

Homo sapiens.

Key	Location/Qualifiers
Modified-site	9 /note= "Phosphorylation site"
Domain	36..55 /label= Transmembrane_domain
Domain	65..84 /label= Transmembrane_domain
Domain	103..130 /label= Transmembrane_domain
Modified-site	108 /note= "Glycosylation site"
Modified-site	130 /note= "phosphorylation site"

WC300012711-A2

09-MAR-2000

02-SEP-1999: 99WO-US020468.

03-SEP-1998. 98US-0155226P.

12-NOV-1998; 38US-00131283;
00-DEC-1998; 98US-0155225P

26-JAN-1999; 0905-0133ZII

PR 10-FEB-1999; 99US-0155263P.
 PA (INCY-) INCYTE PHARM INC.
 XX Au-Young J, Bandman O, Tang YT, Reddy R, Hillman JL, Yue H;
 PI Lal P, Corley NC, Guegler KJ, Gorgone G, Baughn MR, Azimzai Y;
 XX WPI; 2000-256643/22.
 DR N-PSDB; AAZ51624.
 XX Novel human membrane channel protein and polynucleotide useful for
 PT diagnosing and treating cell proliferative, inflammatory, secretory,
 PT osmoregulatory, muscular, cardiovascular and neurological disorders.
 XX Claim 1; Page 107; 140pp; English.
 PS The present sequence is the human membrane channel protein-8 (MECHP-8),
 CC which is expressed in nervous and gastrointestinal tissues. Anti-MECHP
 CC antibodies can be used as therapeutic antagonists and reagents for
 CC diagnosis and monitoring diseases. MECHP cDNA can be used for diagnosis
 CC of MECHP-related diseases and gene mapping. MECHP can be used for
 CC treatment of cell proliferative disorders such as bursitis and
 CC atherosclerosis, cancers like lymphoma and sarcoma, inflammatory
 CC disorders like AIDS and Addison's disease, transport/secretory disorders
 CC like cystic fibrosis and diabetes mellitus, osmoregulatory disorders like
 CC diarrhoea and renal failure, muscular disorders like myocarditis and
 CC Duchenne's muscular dystrophy, cardiovascular disorders like hypertension
 CC and vasculitis, congenital lung anomalies like bronchitis and asthma and
 CC neurological disorders like Alzheimer's disease, Parkinson's disease and
 CC Huntington's disease
 XX Sequence 182 AA;
 SQ Query Match 100.0%; Score 930; DB 3; Length 182;
 Best Local Similarity 100.0%; Pred. No. 1.1e-106;
 Matches 182; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAEPFSKVSTRTSSPAQGAASVSALRDLGFRVSRGLGALMLLQLVLGLLVWALIADTPY 60
 DB 1 MAEPFSKVSTRTSSPAQGAASVSALRDLGFRVSRGLGALMLLQLVLGLLVWALIADTPY 60
 QY 61 HLYPAYGWNMFVAVFLWLVTVILFNLVLFQHLKMLYMPWPLVLMFNISATVLYITAFI 120
 DB 61 HLYPAYGWNMFVAVFLWLVTVILFNLVLFQHLKMLYMPWPLVLMFNISATVLYITAFI 120
 QY 121 ACSAAVDLTSRLGTRFPYNQRAAASFFACLVMIAYGVSAFFSYQAWRGVGSNAATSQMAGG 180
 DB 121 ACSAAVDLTSRLGTRFPYNQRAAASFFACLVMIAYGVSAFFSYQAWRGVGSNAATSQMAGG 180
 QY 181 YA 182
 DB 181 YA 182
 RESULT 2
 ID ADN04054 standard; protein; 182 AA.
 XX ADN04054;
 AC ADN04054;
 XX 01-JUL-2004 (first entry)
 DT Antipsoriatic protein sequence #222.
 DE antipsoriatic; gene therapy; psoriasis; diagnosis.
 KW Homo sapiens.
 XX WO2004028479-A2.
 PN 08-APR-2004.
 PD 25-SEP-2003; 2003WO-US030907.
 PF

XX 25-SEP-2002; 2002US-0414006P.
 XX (GETH) GENENTECH INC.
 PA Bodary S, Clark H, Jackman J, Schoenfeld J, Williams PM, Wood WI;
 PI Wu TD;
 XX WPI; 2004-305105/28.
 DR N-PSDB; ADN04053.
 XX New PRO nucleic acid or polypeptide, useful for preparing a
 PT pharmaceutical composition for diagnosing or treating psoriasis in a
 PT mammal.
 XX Claim 9; SEQ ID NO 448; 3069pp; English.
 PS The invention relates to novel polynucleotide and polypeptides for
 CC treating psoriasis or a sequence having at least 80% identity to the
 CC above sequences. The nucleic acid is useful for preparing a composition
 CC for diagnosing or treating psoriasis in a mammal. This sequence
 CC corresponds to one of the polypeptides of the invention.
 XX Sequence 182 AA;
 SQ Query Match 100.0%; Score 930; DB 8; Length 182;
 Best Local Similarity 100.0%; Pred. No. 1.1e-106;
 Matches 182; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAEPFSKVSTRTSSPAQGAASVSALRDLGFRVSRGLGALMLLQLVLGLLVWALIADTPY 60
 DB 1 MAEPFSKVSTRTSSPAQGAASVSALRDLGFRVSRGLGALMLLQLVLGLLVWALIADTPY 60
 QY 61 HLYPAYGWNMFVAVFLWLVTVILFNLVLFQHLKMLYMPWPLVLMFNISATVLYITAFI 120
 DB 61 HLYPAYGWNMFVAVFLWLVTVILFNLVLFQHLKMLYMPWPLVLMFNISATVLYITAFI 120
 QY 121 ACSAAVDLTSRLGTRFPYNQRAAASFFACLVMIAYGVSAFFSYQAWRGVGSNAATSQMAGG 180
 DB 121 ACSAAVDLTSRLGTRFPYNQRAAASFFACLVMIAYGVSAFFSYQAWRGVGSNAATSQMAGG 180
 QY 181 YA 182
 DB 181 YA 182
 RESULT 3
 ID ADO55157 standard; protein; 182 AA.
 XX ADO55157;
 AC ADO55157;
 XX 15-JUL-2004 (first entry)
 DT Protein #59 with increased gene expression in renal cell carcinoma.
 DE cytostatic; gene therapy; differential expression; renal cell carcinoma;
 KW clear cell RCC; papillary RCC; chromophobe/oncocytoma RCC;
 KW sarcomatoid RCC; TCC; Wilms' tumor; gene expression; kidney cancer;
 KW diagnostic marker; cancer.
 XX Homo sapiens.
 OS WO2004032842-A2.
 XX 22-APR-2004.
 PD 06-OCT-2003; 2003WO-US031476.
 PF 04-OCT-2002; 2002US-0415775P.
 XX (VAND-) VAN ANDEL INST.
 XX

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PI   Teh BT, Takahashi M;
XX   WPI; 2004-340789/31.
DR   N-PSDB; ADO54972.
XX
XX   New nucleic acid and polypeptide compositions, useful in the field of
XX   molecular biology and medicine, in particular for gene expression
XX   profiling, identifying diagnostic markers, and treating certain types of
XX   kidney cancer.
XX
XX   Example IV; SEQ ID NO 254; 53pp; English.
XX
XX   The invention relates to novel genes that are differentially expressed in
XX   sub-types of renal cell carcinomas and methods of detecting them using
XX   nucleic acids and probes. The nucleic acid probes hybridize with part or
XX   all of a coding sequence that is overexpressed in clear cell renal cell
XX   carcinoma (CC-RCC), papillary RCC, chromophobe/oncocytoma RCC,
XX   sarcomatoid RCC, TCC, or Wilms' tumors, which overexpression is based on
XX   comparison to a baseline value. The methods and compositions of the
XX   present invention are useful in the field of molecular biology and
XX   medicine, in particular for gene expression profiling of certain types of
XX   kidney cancer, in identifying diagnostic markers, and treating such
XX   cancer patients. This sequence corresponds to the protein encoded by a
XX   gene with increased expression in CC-RCC.
XX
XX   Sequence 182 AA;
XX
XX   Query Match          100.0%; Score 930; DB 8; Length 182;
XX   Best Local Similarity 100.0%; Pred. No. 1.1e-106;
XX   Matches 182; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX   Qy 1 MAEFPKSVTRTSSPAQGAASVSALRDPDLGFRSRLGALMLLQLVLGLVWALIADTPY 60
XX   Db 1 MAEFPKSVTRTSSPAQGAASVSALRDPDLGFRSRLGALMLLQLVLGLVWALIADTPY 60
XX
XX   Qy 61 HLYPAYGWNMFVAVFLWLVTVILFNLYLFQHLHKLWYWPVPLVLFNLSATVLYITAFI 120
XX   Db 61 HLYPAYGWNMFVAVFLWLVTVILFNLYLFQHLHKLWYWPVPLVLFNLSATVLYITAFI 120
XX
XX   Qy 121 ACSAAVDLTSRLGTRTPYNQRAAASFFACLVMIAYGVSFFSYQAWRGVGSNAATSQMAGG 180
XX   Db 121 ACSAAVDLTSRLGTRTPYNQRAAASFFACLVMIAYGVSFFSYQAWRGVGSNAATSQMAGG 180
XX
XX   Qy 181 YA 182
XX   Db 181 YA 182
XX
XX   RESULT 4
XX   AAB61164
XX   ID AAB61164 standard; protein; 216 AA.
XX   AC AAB61164;
XX   XX
XX   DT 02-APR-2001 (first entry)
XX   DE Human BBSR PLP protein.
XX   KW Human; BBSR; Bardet-Biedl Syndrome Region; PLP; plasmalipin-like protein;
XX   KW antidiabetic; anorectic; ophthalmological; antiinflammatory; nootropic;
XX   KW cardiant; nephrotropic; gene therapy; chromosome 16;
XX   KW retinal degeneration; hypogenitalism; polydactyly; brachydactyly;
XX   KW obesity; mental retardation; renal disorder; diabetes;
XX   KW cardiovascular disorder.
XX   OS
XX   OS Homo sapiens.
XX   FN WO200100825-A2.
XX   XX
XX   PD 04-JAN-2001.
XX   PF 22-JUN-2000; 2000WO-US017375.
XX   XX

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PR 30-JUN-1999; 99US-0141753P.
XX (CHIR ) CHIRON CORP.
XX
XX Duhl D, Gorman SW;
XX
XX WPI; 2001-123009/13.
DR N-PSDB; AAF28357.
XX
XX New human chromosome 15 and 16 Bardet-Biedl Syndrome Region polypeptide
XX and polynucleotide for diagnosis and treatment of obesity, retinal
XX degeneration, mental retardation, nervous system, heart and kidney
XX disorders.
XX
XX Claim 10; Fig 2; Sipp; English.
XX
XX The present sequence is encoded by one of five novel Bardet-Biedl
XX Syndrome Region (BBSR) polynucleotides that map to human chromosome 15 or
XX 16. BBSR polynucleotides, polypeptides and anti-BBSR antibodies are
XX useful for treating a BBSR protein-modulated disorder in a subject. An
XX antibody that specifically binds to a BBSR protein is useful for
XX diagnosing a BBSR protein-modulated disorder. BBSR protein-modulated
XX disorders include Bardet-Biedl syndrome, retinal degeneration including
XX retinitis pigmentosa, hypogenitalism, polydactyly, brachydactyly,
XX obesity, mental retardation, renal abnormalities, diabetes and
XX cardiovascular abnormalities. BBSR polypeptides are also useful for
XX screening combinatorial libraries to identify agonist or antagonists.
XX Antibodies against BBSR polypeptides are useful for affinity
XX chromatography, for distinguishing BBSR polypeptides and for inhibiting
XX or modulating an activity or biological effect of a disorder associated
XX with the BBSR proteins
XX
XX Sequence 216 AA;
XX
XX Query Match          100.0%; Score 930; DB 4; Length 216;
XX   Best Local Similarity 100.0%; Pred. No. 1.4e-106;
XX   Matches 182; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX   Qy 1 MAEFPKSVTRTSSPAQGAASVSALRDPDLGFRSRLGALMLLQLVLGLVWALIADTPY 60
XX   Db 1 MAEFPKSVTRTSSPAQGAASVSALRDPDLGFRSRLGALMLLQLVLGLVWALIADTPY 60
XX
XX   Qy 61 HLYPAYGWNMFVAVFLWLVTVILFNLYLFQHLHKLWYWPVPLVLFNLSATVLYITAFI 120
XX   Db 61 HLYPAYGWNMFVAVFLWLVTVILFNLYLFQHLHKLWYWPVPLVLFNLSATVLYITAFI 120
XX
XX   Qy 121 ACSAAVDLTSRLGTRTPYNQRAAASFFACLVMIAYGVSFFSYQAWRGVGSNAATSQMAGG 180
XX   Db 121 ACSAAVDLTSRLGTRTPYNQRAAASFFACLVMIAYGVSFFSYQAWRGVGSNAATSQMAGG 180
XX
XX   Qy 181 YA 182
XX   Db 181 YA 182
XX
XX   RESULT 5
XX   AAR99799
XX   ID AAR99799 standard; protein; 182 AA.
XX   AC AAR99799;
XX   DT 25-MAR-2003 (revised)
XX   DT 02-JAN-1997 (first entry)
XX   DE NTII-11 nerve protein, facilitates regeneration of nerve cells.
XX   KW Probe; central nervous system; peripheral nervous system; CNS; PNS; axon;
XX   KW neurone; neuronal cells; glial cells; Schwann cells; trauma; pathology;
XX   KW regeneration; MS2; metalloprotease.
XX   OS
XX   OS Homo sapiens.
XX   FN WO9617865-A2.
XX

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XX 13-JUN-1996.
 XX 05-DEC-1995; 95WO-EP004777.
 XX 05-DEC-1994; 94DE-04443159.
 PR 27-JAN-1995; 95DE-01002525.
 XX (BOEF) BOEHRINGER MANNHEIM GMBH.
 XX
 PI Mueller H, Gillen C, Gleichmann M;
 XX WPI; 1996-287114/29.
 DR N-PSDB; AAT34592.
 XX
 PT Nucleic acids associated with damaged or regenerating nerve cells - for
 PT diagnostic or therapeutic use.
 XX
 PS Claim 4; Page 45-46; 54pp; German.
 XX
 CC Nucleic acids described in AAT34587-T34616 are useful as probes for
 CC detecting traumatic and pathological changes in the peripheral nervous
 CC system. They may also be used to identify hybridising sequences from an
 CC ischial nerve cDNA library, these sequences encode proteins expressed in
 CC damaged and/or regenerating nerve cells. They can be used to transfect
 CC cells which then express the protein which can then be harvested and
 CC studied. The nucleic acids are preferably selected from NTII-11 which
 CC corresponds to plasmolipin cDNA with a 234 bp N-terminal extension and is
 CC expressed in glial cells of the central nervous system and Schwann cells
 CC of the peripheral nervous system; NTII-1, which codes for this protein
 CC having 79% homology with human CDC4L in three domains and may be involved
 CC in regulating Schwann cell growth as well as being therapeutically useful
 CC for regenerating nerve cells; and CR11-7 which codes for a protein which
 CC is similar to the macrophage-specific cysteine-rich mouse protein MS2 and
 CC a metalloprotease and which inhibits interaction between Schwann cells
 CC and the extracellular matrix and is useful for the therapy of nerve
 CC damage by facilitating regeneration of damaged axons. (Updated on 25-MAR-
 CC 2003 to correct PR field.)
 XX
 SQ Sequence 182 AA;
 Query Match 91.2%; Score 848; DB 2; Length 182;
 Best Local Similarity 88.5%; Pred. No. 1.6e-96;
 Matches 161; Conservative 13; Mismatches 8; Indels 0; Gaps 0;
 QY 1 MAEFPKSVTRTSSPAQGAASVSALRPDLGFRSRLGALMLQLVLGLLWALIADTPY 60
 Db 1 MAEFPKSVTRTSSPAQGVGSASVAMRDLGFRSRLGALMLQLVLGLLWALIADTPY 60
 QY 61 HLYPAYGWMFVAVFLWLVITVLFNLYLFQLMKLYMVPWPLVLMFNISATVLYITAFI 120
 Db 61 HLYPAYGWMFVAVFLWLVITVLFNLYLFQLMKLYMVPWPLVLMFNISATVLYITAFV 120
 QY 121 ACSAAVDLTSLRGTPYRNORAAAPFACLVMIAYGLSAFFSFQAWRGVGSNAATSQMA 180
 Db 121 ACSAAVDLTSLRGTPYRNORAAAPFACLVMIAYGLSAFFSFQAWRGVGSNAATSQMA 180
 QY 181 YA 182
 Db 181 YS 182
 RESULT 6
 ABB90064
 ID ABB90064 standard; protein; 125 AA.
 XX
 AC ABB90064;
 XX
 DT 24-MAY-2002 (first entry)
 XX
 DE Human polypeptide SEQ ID NO 2440.
 XX
 KW Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;

KW antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer;
 KW vulnary; anticonvulsant; antifungal; antifungal; antiparasitic;
 KW cardiatic; gene therapy; cancer; immune disorder; cardiovascular disorder;
 XX neurological disease; infection; human; secreted protein.
 OS Homo sapiens.
 XX WO200190304-A2.
 PN 29-NOV-2001.
 PD 18-MAY-2001; 2001WO-US016450.
 PP 19-MAY-2000; 2000US-0205515P.
 PR (HUMA-) HUMAN GENOME SCI INC.
 XX Birse CE, Rosen CA;
 PI WPI: 2002-122018/16.
 DR N-PSDB; ABL90473.
 XX Novel 1405 isolated polypeptides, useful for diagnosis, treatment and
 PT prevention of neural, immune system, muscular, reproductive,
 PT gastrointestinal, pulmonary, cardiovascular, renal and proliferative
 PT disorders.
 XX
 PS Claim 11; SEQ ID NO 2440; 2081pp + Sequence Listing; English.
 XX The invention relates to novel genes (ABL89449-ABL90853) and proteins
 CC (ABB89040-ABB90444) useful for preventing, treating or ameliorating
 CC medical conditions e.g. by protein or gene therapy. The genes are
 CC isolated from a range of human tissues disclosed in the specification.
 CC The nucleic acids, proteins, antibodies and (ant)agonists are useful in
 CC the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and
 CC ovarian cancer and other cancers of the adrenal gland, bone, bone marrow,
 CC breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune
 CC disorders e.g. Addison's disease, allergies, autoimmune haemolytic
 CC anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,
 CC multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c)
 CC cardiovascular disorders such as myocardial ischaemias; (d) wound healing
 CC ; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f)
 CC infectious diseases such as viral, bacterial, fungal and parasitic
 CC infections. Note: The sequence data for this patent did not form part of
 CC the printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 125 AA;
 Query Match 67.2%; Score 625; DB 5; Length 125;
 Best Local Similarity 97.6%; Pred. No. 4.6e-69;
 Matches 122; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 MAEFPKSVTRTSSPAQGAASVSALRPDLGFRSRLGALMLQLVLGLLWALIADTPY 60
 Db 1 MAEFPKSVTRTSSPAQGAASVSALRPDLGFRSRLGALMLQLVLGLLWALIADTPY 60
 QY 61 HLYPAYGWMFVAVFLWLVITVLFNLYLFQLMKLYMVPWPLVLMFNISATVLYITAFI 120
 Db 61 HLYPAYGWMFVAVFLWLVITVLFNLYLFQLMKLYMVPWPLVLMFNISATVLYITAFI 120
 QY 121 ACSAA 125
 Db 121 GCSAA 125
 RESULT 7
 AAB34711
 ID AAB34711 standard; protein; 113 AA.
 XX
 AC AAB34711;
 XX
 DT 26-JAN-2001 (first entry)

XX DE Human secreted protein encoded by DNA clone v06.1.

XX KW Secreted protein; human; autoimmune disorder; multiple sclerosis; ulcer;

XX KW systemic lupus erythematosus; rheumatoid arthritis; anaemia; stroke;

XX KW haematopoiesis regulation; tissue regrowth; wound healing; haemophilia;

XX KW Alzheimer's disease; Parkinson's disease; Shy-drager syndrome; cancer;

XX KW contraceptive; infection; growth inhibition; hyperproliferative disorder;

XX KW psoriasis.

XX OS Homo sapiens.

XX PN WO200055375-A1.

XX PD 21-SEP-2000.

XX PF 17-MAR-2000; 2000WO-US007285.

XX PR 17-MAR-1999; 99US-0124808P.

XX PR 17-MAR-1999; 99US-0124916P.

XX PR 17-AUG-1999; 99US-0149639P.

XX PR 01-OCT-1999; 99US-0157247P.

XX PR 29-NOV-1999; 99US-0167824P.

XX PR 15-FEB-2000; 2000US-0182711P.

XX PA (ALPH-) ALPHAGENE INC.

XX PI Valenzuela D, Yuan O, Hoffman H, Hall J, Rapiejko P;

XX DR WPI; 2000-638211/61.

XX DR N-PSDB; AAC59812.

XX PT Novel proteins and polypeptides useful for the treatment of e.g multiple

XX PT sclerosis, systemic lupus erythematosus, rheumatoid arthritis, cancer,

XX PT Alzheimer's disease, Parkinson's disease, stroke, anemia and ulcers.

XX PS Claim 58; Page 419; 493pp; English.

XX CC This invention relates to 59 human secreted proteins and the nucleotide

XX CC sequences encoding them. Sequences AAC59788-C59846 and AAB34687-B34745

XX CC represent the proteins and their encoding nucleotide sequences, and

XX CC sequences AAB34746-B34771 represent fragments of the proteins. Probes for

XX CC the DNA sequences are represented by sequences AAC59847-C59996. The

XX CC proteins exhibit neuroprotective, dermatological, immunosuppressive,

XX CC antiinflammatory, antianaemic, neurotropic, antiparkinsonian,

XX CC cerebroprotective, haemostatic, vulnary, cytostatic, antipsoriatic,

XX CC antibacterial, virucide, and fungicide activity. The proteins and

XX CC nucleotide sequences are useful as nutritional sources or supplements and

XX CC in research. The proteins are useful for treating immune deficiency and

XX CC disorders, which may be genetic or resulting from infections, autoimmune

XX CC disorders such as multiple sclerosis, systemic lupus erythematosus,

XX CC rheumatoid arthritis, and for treating myeloid or lymphoid cell

XX CC deficiencies such as anaemias by regulating haematopoiesis. The proteins

XX CC are also useful in compositions for bone, cartilage, tendon, ligament

XX CC and/or nerve tissue growth or regeneration, for wound healing, tissue

XX CC repair and replacement and in the treatment of wounds, incisions and

XX CC ulcers. Other uses include in the treatment of central and peripheral

XX CC nervous system and neuropathies such as Alzheimer's and Parkinson's

XX CC diseases and Shy-drager syndrome, and mechanical and traumatic disorders,

XX CC such as spinal cord disorders, head trauma and stroke. The proteins may

XX CC also be used as a contraceptive and for treating coagulation disorders

XX CC such as haemophilias. The protein and nucleotide sequences with cadherin

XX CC activity are useful for treating cancer. Other uses for the protein

XX CC include for inhibiting the growth, infection or function of, or killing,

XX CC infectious agents such as bacteria, virus, fungi and other parasites, for

XX CC effecting bodily characteristics such as height, weight, hair colour,

XX CC effecting biorhythms or cardiac cycles or rhythms, effecting metabolism,

XX CC catabolism, anabolism, processing, utilization, storage or elimination of

XX CC dietary fat, lipid, protein, carbohydrate, vitamins, minerals, cofactors,

XX CC effecting behavioural characteristics, providing analgesic effects and

XX CC for treating hyperproliferative disorders such as psoriasis

XX CC Sequence 113 AA;

XX SQ

Query Match 62.4%; Score 580; DB 3; Length 113;
 Best Local Similarity 100.0%; Pred. No. 1.5e-63;
 Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 70 MFVAVFLMTVTLVNLVLFQHLHMLYMPVPLVLMINISATVLYITAFIACSAVDLT 129
 |||||
 Db 1 MFVAVFLMTVTLVNLVLFQHLHMLYMPVPLVLMINISATVLYITAFIACSAVDLT 60
 |||||

QY 130 SLRGTPTNORAAAFACLVMIAYGVSAFFSYQAWRGVGSNAATSQAGGYA 182
 |||||
 Db 61 SLRGTPTNORAAAFACLVMIAYGVSAFFSYQAWRGVGSNAATSQAGGYA 113
 |||||

RESULT 8
 ABB90110
 ID ABB90110 standard; protein; 113 AA.
 XX AC ABB90110;
 XX DT 24-MAY-2002 (first entry)
 XX DE Human polypeptide SEQ ID NO 2486.
 XX KW Cytostatic; immunosuppressive; neurotropic; neuroprotective; antiviral;
 KW anti-allergic; hepatotropic; antidiabetic; anti-inflammatory; anti-ulcer;
 KW vulnary; anticonvulsant; antibacterial; antifungal; antiparasitic;
 KW cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;
 KW neurological disease; infection; human; secreted protein.
 XX OS Homo sapiens.
 XX WO200190304-A2.
 XX PD 29-NOV-2001.
 XX PF 18-MAY-2001; 2001WO-US016450.
 XX PR 19-MAY-2000; 2000US-0205515P.
 XX PA (HUMA-) HUMAN GENOME SCI INC.
 XX PI Birse CE, Rosen CA;
 XX WPI; 2002-122018/16.
 XX DR N-PSDB; ABL90519.
 XX PT Novel 1405 isolated polypeptides, useful for diagnosis, treatment and
 PT prevention of neural, immune system, muscular, reproductive,
 PT gastrointestinal, pulmonary, cardiovascular, renal and proliferative
 PT disorders.
 XX PS Claim 11; SEQ ID NO 2486; 2081pp + Sequence Listing; English.

The invention relates to novel genes (ABL99449-ABL90853) and proteins (ABB89040-ABB90444) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemia; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and parasitic infections. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

Query Match 62.4%; Score 580; DB 5; Length 113;
 Best Local Similarity 100.0%; Pred. No. 1.5e-63;
 Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 70 MFVAVFLMLTVLTVLNLVLFQLEHMLVWVPLVLMFNISATVLYITAFIACSAVDLT 129
 DQ 1 MFVAVFLMLTVLTVLNLVLFQLEHMLVWVPLVLMFNISATVLYITAFIACSAVDLT 60
 QY 130 SLRGTREYNQRAAASFFACLVMIAYGVSAFFSYQAMRGVGSNAATSQMAGGYA 182
 DQ 61 SLRGTREYNQRAAASFFACLVMIAYGVSAFFSYQAMRGVGSNAATSQMAGGYA 113

RESULT 9
 AAY53643
 ID AAY53643 standard; protein; 173 AA.
 AC AAY53643;
 DT 22-FEB-2000 (first entry)
 DE A bone marrow secreted protein designated BMS6.
 KW Bone marrow secreted protein; bone marrow stromal cell; cytokine;
 KW cell proliferation; cell differentiation; hematopoiesis; anaemia;
 KW myeloid cell deficiency; lymphoid cell deficiency; myeloid cell;
 KW erythroid progenitor cell; colony stimulating factor; granulocyte;
 KW monocyte; macrophage; myelo-suppression; megakaryocyte; platelet;
 KW platelet disorder; thrombocytopenia; hematopoietic stem cell;
 KW stem cell disorder; aplastic anaemia; bone differentiation;
 KW paroxysmal nocturnal hemoglobinuria; bone growth; cartilage; tendon;
 KW ligament; nerve; wound healing; tissue repair; burn; incision; ulcer;
 KW bone fracture; cartilage damage; artificial joint.
 OS Homo sapiens.
 XX
 XX
 XX WO9933979-A2.
 XX
 XX 08-JUL-1999.
 XX
 XX 18-DEC-1998; 98WO-US027008.
 XX
 XX 20-DEC-1997; 97US-0068958P.
 XX 24-SEP-1998; 98US-0101603P.
 XX 30-SEP-1998; 98US-0102540P.
 XX
 XX (CHIR) CHIRON CORP.
 XX
 XX Lin H, Cao L;
 XX WPI; 2000-038344/03.
 XX N-PSDB; AA236249.
 XX
 XX New isolated human polynucleotide and secreted proteins can induce
 XX production of other cytokines in certain cell populations.
 XX
 XX Claim 2; Page 119; 120pp; English.

AA53622-43 represent bone marrow secreted proteins of human bone marrow
 stromal cells. The proteins can exhibit cytokine, cell proliferation, or
 cell differentiation activity (either inducing or inhibiting). They can
 be used to support colony forming cells or factor-dependent cell lines,
 to regulate hematopoiesis, and to treat myeloid or lymphoid cell
 deficiencies. In addition, they may be used to support the growth and
 proliferation of erythroid progenitor cells, and to treat various
 anaemias. They can have colony stimulating factor (CSF) activity and can
 be used to support the growth and proliferation of myeloid cells such as
 granulocytes, monocytes or macrophages, to prevent or treat myelo-
 suppression, to support the growth and proliferation of megakaryocytes
 and platelets, thereby allowing prevention or treatment of platelet
 disorders such as thrombocytopenia, to support the growth and
 proliferation of hematopoietic stem cells, either in place of or in

conjunction with platelet transfusions, to treat stem cell disorders,
 such as aplastic anaemia and paroxysmal nocturnal hemoglobinuria, or to
 repopulate the stem cell compartment after irradiation or chemotherapy.
 CC They can be used for growth or differentiation of bone, cartilage,
 CC tendon, ligament, or nerve tissue, as well as for wound healing and
 CC tissue repair and replacement, and in the treatment of burns, incisions
 CC and ulcers, to induce cartilage and/or bone growth in circumstances where
 CC bone is not normally formed and thus have an application in healing bone
 CC fractures and cartilage damage or defects, prophylactic use in fracture
 CC reduction and also in the improved fixation of artificial joints
 XX
 XX Sequence 173 AA;

Query Match 34.9%; Score 325; DB 3; Length 173;
 Best Local Similarity 43.8%; Pred. No. 1.1e-31;
 Matches 71; Conservative 29; Mismatches 54; Indels 8; Gaps 2;
 QY 8 VSTRSSPAQGAASVSALRDLGFSRLGALMLLQVLGLVLLVWALIADTPHLYPAYG 67
 DQ 12 VTTTASSFAENSTSSSFAYDREFLTPGLFVABIVLGLVLLVWALIADTPHLYPAYG 71
 QY 68 WMFVAVFLMLTVLTVLNLVLFQLEHMLVWVPLVLMFNISATVLYITAFIACSAVD 127
 DQ 72 WMFVAVFLMLTVLTVLNLVLFQLEHMLVWVPLVLMFNISATVLYITAFIACSAVD 126
 QY 128 LTSL--RGTRPYNQRAAASFFACLVMIAYGVSAFFSYQAMR 166
 DQ 127 ASSVSPDRSHNFSNAASSFFAFVLTICVAGNTYFSFIAMR 168

RESULT 10
 AAM25799
 ID AAM25799 standard; protein; 173 AA.
 AC AAM25799;
 XX
 XX 16-OCT-2001 (first entry)
 XX
 XX Human protein sequence SEQ ID NO:1314.
 XX
 XX Human; cancer; ulcer; HIV infection; human immunodeficiency virus;
 KW antinflammatory; antirheumatic; antiarthritic; immunosuppressive;
 KW antibacterial; endocrine; cardiant; central nervous system; virucide;
 KW anti-HIV; fungicide; antimutagen; cardiovascular; antianaemic; anaemia;
 KW antiaggregant; haemostatic; vulnerary; antilucer; osteopathic; eczema;
 KW dermatological; antiallergic; antisthmatic; antidiabetic; cytostatic;
 KW neuroprotective; antidepressant; nootropic; antiparkinsonian; infection;
 KW immunostimulant; gene therapy; antisense therapy; vaccine; inflammation;
 KW antianaphylactic; rheumatoid arthritis; septic shock; pancreatitis;
 KW cardiac dysfunction; neuropathology; cardiac anaphylaxis; autoimmunity;
 KW genetic disease; haematopoietic disorder; platelet disorder; asthma;
 KW thrombocytopenia; osteoporosis; severe combined immunodeficiency;
 KW allergic rhinitis; diabetes; multiple sclerosis; depression;
 KW Alzheimer's disease; Parkinson's disease; neurodegenerative disorder;
 KW neurological disorder.

OS Homo sapiens.
 XX
 XX WO200153455-A2.
 XX
 XX 26-JUL-2001.
 XX
 XX 22-DEC-2000; 2000WO-US035017.
 XX
 XX 23-DEC-1999; 99US-00471275.
 XX 21-JAN-2000; 2000US-00488725.
 XX 25-APR-2000; 2000US-00552317.
 XX
 XX (HYSE-) HYSEQ INC.
 XX
 XX Tang YT, Liu C, Drmanac RT;
 XX WPI; 2001-457603/49.
 XX

PN N-PSDB; AAH99740.
XX Isolated human polynucleotides encoding polypeptides, useful for the
PT treatment and diagnosis of e.g. cancer, ulcers and HIV infection.
PF Claim 20; Page 273; 1217pp; English.
XX
XX AAH99166 to AAH99904 encode the human proteins given in AAM25225 to
CC AAM25963. The proteins can have activities based on the tissues and cells
CC they are expressed in, such as: antiinflammatory; antirheumatic;
CC antithrombotic; immunosuppressive; antibacterial; endocrine; cardiant;
CC central nervous system; virucide; anti-HIV; fungicide; antimutagen;
CC cardiovascular; antianaemic; antiaggregant; haemostatic; vulnerary;
CC antitumor; osteopathic; dermatological; antiallergic; antiasthmatic;
CC antidiabetic; cytostatic; neuroprotective; antidepressant; nootropic;
CC antiparkinsonian; and immunostimulant. The proteins and polynucleotides
CC encoding them can be used in gene therapy, antisense therapy and vaccine
CC production. The proteins and polynucleotides are useful for screening for
CC agonists or antagonists of a protein and for the treatment and diagnosis
CC of disorders associated with the activity of a protein e.g. inflammation,
CC rheumatoid arthritis, septic shock, pancreatitis, cardiac dysfunction,
CC neuropathology, cardiac anaphylaxis, viral, bacterial, HIV and fungal
CC infections, autoimmunity, genetic diseases, haematopoietic disorders,
CC anaemia, platelet disorders, thrombocytopaenia, wounds, burns, ulcers,
CC osteoporosis, severe combined immunodeficiency, eczema, allergic
CC rhinitis, asthma, diabetes, cancer, multiple sclerosis, depression,
CC Alzheimer's disease, Parkinson's disease, neurodegenerative and
CC neurological disorders
XX
SQ Sequence 173 AA;
Query Match 34.6%; Score 322; DB 4; Length 173;
Best Local Similarity 42.4%; Pred. No. 2.7e-31;
Matches 70; Conservative 30; Mismatches 57; Indels 8; Gaps 2;
QY 5 PSKVRTRTSSPAQGAASVSALRPLDGFVRSRLGALMLQLVGLVWALVADTPYHLYP 64
Db 9 PNAGTRKYSVPALSVHTSSSSSFAYDREPLRTLPGLVIAEIVLGLVWTLVLTAGTEYFRVP 68
QY 65 AYGVNMFVAVLWLVTVTFNLYFQLHMKLVMPVPLVLMFNISATVLYITAFIACSA 124
Db 69 AFGVNMFAVAVVWLVTVTFNLYFQLHMKLVMPVPLVLMFNISATVLYITAFIACSA 123
QY 125 AVDLTSL---RGTRPNORAAASFFACLVMIAYGVSAFYSQAWR 166
Db 124 VVDASSVSPERDHNFNWSAASSFFAFLVTCIAGNTYFSAFIAWR 168
RESULT 11
ID AAW52117 standard; protein; 153 AA.
XX
AC AAW52117;
XX
DT 07-JUL-1998 (first entry)
XX
XX Human proteolipid (PLHu) protein.
DE
XX Human proteolipid; PLHu; exocytosis; membrane trafficking;
KW rat plasmolipin; chemokine; inflammation.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
FH Domain 20..40
FT /note= "Transmembrane domain 1"
FT 50..72
FT /note= "Transmembrane domain 2"
FT 84..108
FT /note= "Transmembrane domain 3"
FT 127..147
FT /note= "Transmembrane domain 4"
XX

PN WO9804691-A1.
XX
PD 05-FEB-1998.
XX
PF 21-JUL-1997; 97WO-US012734.
XX
XX 26-JUL-1996; 96US-00695736.
XX
XX (INCY-) INCYTE PHARM INC.
XX
XX Au-Young J, Bandman O, Goli SK, Hillman JL;
PI WPI; 1998-130683/12.
XX
XX N-PSDB; AAV17143.
XX
XX Human proteolipid PLHu - used to accelerate diagnosis and proper
PT treatment of diseases and conditions associated with abnormal membrane
PT trafficking.
XX
XX Claim 1; Fig 1A-1B; 53pp; English.
XX
XX The present sequence is of a human proteolipid (PLHu) protein which was
CC expressed by PLHu cDNA of the current invention. A partial sequence of
CC PLHu cDNA was initially isolated as incyte clone 640699 derived from a
CC human breast cDNA library. Homology of PLHu protein to rat plasmolipin
CC indicates its involvement in exocytosis. Exocytosis facilitated by PLHu
CC may influence membrane trafficking within the cell and could affect the
CC release of chemokines involved in cell migration, proteases which are
CC active in inflammation or other similar activities involving endothelial
CC cells, fibroblasts, etc. The invention also claims for antibodies against
CC PLHu which can be used for e.g. in diagnostic tests to accelerate
CC diagnosis and proper treatment of conditions associated with abnormal
CC membrane trafficking
XX
XX Sequence 153 AA;
Query Match 33.0%; Score 307; DB 2; Length 153;
Best Local Similarity 44.6%; Pred. No. 1.7e-29;
Matches 66; Conservative 27; Mismatches 47; Indels 8; Gaps 2;
QY 22 SVSALRPLDGFVRSRLGALMLQLVGLVWALVADTPYHLYPAYGVNMFVAVFLMLVTI 81
Db 6 SSSSFAYDREPLRTLPGLVIAEIVLGLVWTLVLTAGTEYFRVPAFGVNMFAVAVVWLVTV 65
QY 82 VLFNLYFQLHMKLVMPVPLVLMFNISATVLYITAFIACSAVDLTSL---RGTRPN 138
Db 66 FFLIYITMTYTRIPQVPTVTVGLCFNGSAFVLYLSA-----AVVDASSVSPERDHNFN 120
QY 139 QRAAASFFACLVMIAYGVSAFYSQAWR 166
Db 121 SWAASSFFAFLVNICYAGNTYFSAFIAWR 148
RESULT 12
ABP41095
ID ABP41095 standard; protein; 132 AA.
XX
XX AC ABP41095;
XX
XX 22-AUG-2002 (first entry)
XX
XX Human ovarian antigen HSAVH65, SEQ ID NO:2227.
XX
XX Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;
KW ovarian cancer; breast cancer; tumour; reproductive system disorder;
KW infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;
KW PCOS; ovarian cyst; dysmenorrhea; endocrine disorder; infection;
KW inflammatory condition; immune disorder; blood disorder;
KW cardiovascular disorder; respiratory disorder; neurological disorder;
KW gastrointestinal disorder; urinary system disorder; drug screening;
KW gene therapy; chromosome mapping; forensic analysis;
KW antibody preparation; cytostatic; immunomodulatory; neuroprotective;
KW antiinflammatory; gynaecological; reproductive.

ADA57177
ID ADA57177 standard; protein; 100 AA.
XX
AC ADA57177;
XX
20-NOV-2003 (first entry)
DT
XX
DE Human secreted protein #460.
XX
XX immunosuppressive; antiinflammatory; antiasthmatic; antiallergic;
KW cytostatic; cerebroprotective; neuroprotective; nootropic;
KW cardiovascular; antiarteriosclerotic; gene therapy;
KW human secreted protein; immune disorder; inflammation;
KW respiratory disorder; cancer; CNS disorder; neurodegenerative disorders;
KW inflammatory bowel disease; nephritis; Crohn's disease; asthma; allergy;
KW multiple sclerosis; ischaemic brain injury; Parkinson's disease;
KW Alzheimer's disease; atherosclerosis; myocarditis; chromosome mapping;
KW triple helix formation; antisense gene therapy; forensic biology.
XX
OS Homo sapiens.
XX
XX WO2002102994-A2.
PN
XX
XX 27-DEC-2002.
PD
XX
XX 19-MAR-2002; 2002WO-US008278.
PF
XX
XX 21-MAR-2001; 2001US-0277340P.
PR
XX 19-JUL-2001; 2001US-0306171P.
PR
XX 13-NOV-2001; 2001US-0331287P.
PR
XX (HUMA-) HUMAN GENOME SCI INC.
PA
XX
XX Rosen CA, Ruben SM;
PI
XX WPI; 2003-167512/16.
DR
XX N-PSDB; ADA56281.
DR
XX
XX New human secreted polypeptides and polynucleotides, useful for
PT diagnosing, treating or preventing e.g. immune disorders, inflammatory
PT conditions, respiratory disorders, cancers, CNS disorders, or
PT neurodegenerative disorders.
PT
XX
XX Claim 13; SEQ ID NO 1367; 1754pp; English.
PS
XX
XX The invention relates to 592 new human secreted polypeptides useful for
CC diagnosing, treating or preventing e.g. immune disorders, inflammatory
CC conditions, respiratory disorders, cancers, CNS disorders, or
CC neurodegenerative disorders, or polypeptides comprising an amino acid
CC sequence at least 95% identical to the new sequences. The polypeptides,
CC antibodies or antibody fragments that bind to the polypeptides, nucleic
CC acids encoding the polypeptides, agonists or antagonists that binds to
CC the polypeptide, are useful in preparing diagnostic or pharmaceutical
CC compositions for diagnosing, treating or preventing an e.g. immune
CC disorders, inflammatory conditions (e.g. inflammatory bowel disease,
CC nephritis or Crohn's disease), respiratory disorders (e.g. asthma and
CC allergy), cancers (e.g. gastric, ovarian or lung cancer), CNS disorders
CC (e.g. multiple sclerosis or ischaemic brain injury), neurodegenerative
CC disorders (e.g. Parkinson's disease or Alzheimer's disease), and
CC cardiovascular disorders (e.g. atherosclerosis or myocarditis). The
CC polynucleotides are useful for chromosome identification, chromosome
CC mapping, for controlling gene expression through triple helix formation
CC or antisense DNA or RNA, in gene therapy, for identifying individuals
CC from minute biological samples, in forensic biology, and as hybridization
CC probes. The polypeptides are useful for as molecular weight markers on
CC sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE)
CC gels, to raise antibodies, for testing biological activities, and for
CC treating or preventing neural disorders, immune system disorders,
CC muscular, reproductive, gastrointestinal, pulmonary, cardiovascular,
CC renal, proliferative and/or cancerous diseases. This sequence corresponds
CC to one of the polypeptide of the invention. Note: The sequence data for
CC this patent did form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at

ftp.wipo.int/pub/published_pct_sequences.
CC
XX Sequence 100 AA;
SQ
Query Match 20.5%; Score 191; DB 6; Length 100;
Best Local Similarity 41.0%; Pred. No. 2.3e-15;
Matches 41; Conservative 20; Mismatches 31; Indels 8; Gaps 2;
QY 70 MFVAVFVLTIVLVFNLYLQLHMKLYMPVPLVLMFNISATVLYITAFIACSAADLT 129
DB 1 MFVAVFVLTIVLVFNLYLQLHMKLYMPVPLVLMFNISATVLYITAFIACSAADLT 129
QY 130 SL---RGRTPYNQRAAASFACLVMIAYGVSAFFSYQAWR 166
DB 56 SVSEKDSHNFNSWAASSFFAFLVTCYAGNTYFSEFXAWR 95
RESULT 15
ADA41044
ID ADA41044 standard; protein; 100 AA.
XX
AC ADA41044;
XX
XX 20-NOV-2003 (first entry)
DT
XX
XX Human secreted protein.
DE
XX
XX Human; secreted protein; cancer; hyperproliferative disorder;
KW rheumatoid arthritis; autoimmune disorder; haematopoietic disorder;
KW anaemia; allergic reaction; asthma; cardiovascular disorder;
KW wound healing; cytostatic; immunosuppressive; nootropic; neuroprotective;
KW antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory;
KW vulnery; cardiant; gene therapy.
XX
XX Homo sapiens.
OS
XX
XX WO2002102993-A2.
PN
XX
XX 27-DEC-2002.
PD
XX
XX 19-MAR-2002; 2002WO-US008123.
PF
XX
XX 21-MAR-2001; 2001US-0277340P.
PR
XX 19-JUL-2001; 2001US-0306171P.
PR
XX 13-NOV-2001; 2001US-0331287P.
PR
XX (HUMA-) HUMAN GENOME SCI INC.
PA
XX
XX Rosen CA, Ruben SM;
PI
XX WPI; 2003-175238/17.
DR
XX
XX New human secreted proteins and nucleic acid molecules, useful for
PT preparing a diagnostic or pharmaceutical composition for diagnosing,
PT preventing or treating cancer or other hyperproliferative disorder,
PT asthma, allergies or AIDS.
PT
XX
XX Claim 1; SEQ ID NO 1426; 3205pp; English.
PS
XX
XX The invention relates to novel genes ADA39629-ADA40565 and proteins
CC ADA40566-ADA41501 for human secreted proteins, useful for preventing,
CC treating or ameliorating medical conditions e.g. by protein or gene
CC therapy. The polypeptides, nucleic acid molecules, antibodies or their
CC fragments, and agonists or antagonists that bind to the polypeptide are
CC useful for preparing a diagnostic or pharmaceutical composition for
CC diagnosing or treating cancer or other hyperproliferative disorder. The
CC polypeptides and nucleic acid molecules are also useful for detecting,
CC preventing, diagnosing, prognosticating, treating or ameliorating cancer
CC or other hyperproliferative disorders including neoplasms, autoimmune
CC disorders (e.g. diabetes, rheumatoid arthritis, systemic lupus
CC erythematosus, multiple sclerosis, autoimmune thyroiditis or haemolytic
CC anaemia), haematopoietic or haematological disorders (e.g. anaemia,
CC thrombocytopenia), allergic reactions including asthma or eczema,

CC inflammatory disorders (e.g. ischaemia-reperfusion injury, inflammatory
 CC bowel disease or Crohn's disease), neurodegenerative disorders (e.g.
 CC Alzheimer's disease or Parkinson's disease), cardiovascular disorders
 CC (e.g. atherosclerosis, myocarditis), infectious diseases (bacterial,
 CC fungal or viral infections including HIV/AIDS), or wound healing and
 CC disorders of epithelial cell proliferation. The nucleic acids are also
 CC useful for chromosome identification, radiation hybrid mapping or long-
 CC range restriction mapping, as molecular weight markers, or as
 CC hybridization or diagnostic probes. The polypeptides and antibodies are
 CC useful for providing immunological probes for differential identification
 CC of the tissues immunohistochemistry assays. Note: The sequence data for
 CC this patent did not form part of the printed specification, but was
 CC obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX
 XX
 SQ Sequence 100 AA;

Query Match 20.5%; Score 191; DB 6; Length 100;
 Best Local Similarity 41.0%; Pred. No. 2.3e-15;
 Matches 41; Conservative 20; Mismatches 31; Indels 8; Gaps 2;
 Qy 70 MFVAVFLWLTIVLFLNLYLFLQHNKLYWEPPLVLMFNISATVLYITAFIACSAAYDLT 129
 Db 1 MFVAVFLWLTIVLFLNLYLFLQHNKLYWEPPLVLMFNISATVLYITAFIACSAAYDLT 129
 Qy 130 SL---RGTRPYNQRAAASFFACLVMIAAYGVSAFFSYQAWR 166
 Db 56 SVSPKDSHNFNNSWAASSFFAFLVTCYAGNTYFSFXAWR 95

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 Job time : 159 secs

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OM protein - protein search, using sw model

Run on: December 1, 2004, 15:29:28 ; Search time 40 Seconds
(without alignments)
301.747 Million cell updates/sec

Title: US-09-602-597A-4
Perfect score: 930
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Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: /cgn2_6/prodata/1/aa/6A-COMB.pep: *
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5: /cgn2_6/prodata/1/aa/PCrUS-COMB.pep: *
6: /cgn2_6/prodata/1/aa/backfiles1.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	741	79.7	157	US-08-695-736-3	Sequence 3, Appli
2	307	33.0	153	US-08-695-736-1	Sequence 1, Appli
3	153	16.5	153	US-08-695-736-4	Sequence 4, Appli
4	148.5	16.0	148	US-09-702-705-338	Sequence 338, App
5	148.5	16.0	148	US-09-736-457-338	Sequence 338, App
6	148.5	16.0	148	US-09-614-124B-338	Sequence 338, App
7	148.5	16.0	148	US-09-671-325-338	Sequence 338, App
8	148.5	16.0	148	US-09-589-184-338	Sequence 338, App
9	148.5	16.0	148	US-09-558-824-338	Sequence 338, App
10	127.5	13.7	299	US-09-520-781-28	Sequence 28, Appl
11	91	9.8	421	US-09-198-452A-932	Sequence 932, App
12	88.5	9.5	220	US-09-328-714A-4	Sequence 4, Appli
13	88	9.5	296	US-09-107-532A-6356	Sequence 6356, Ap
14	87	9.4	448	US-09-328-352-5694	Sequence 5694, Ap
15	86.5	9.3	211	US-09-352-991A-23822	Sequence 23822, A
16	86.5	9.3	289	US-09-724-864-47	Sequence 47, Appl
17	86.5	9.3	400	US-07-916-901-6	Sequence 6, Appli
18	86.5	9.3	400	US-07-783-602C-1	Sequence 1, Appli
19	86.5	9.3	400	US-08-351-473B-4	Sequence 4, Appli
20	85	9.1	446	US-09-352-991A-22844	Sequence 22844, A
21	84.5	9.1	378	US-09-560-761-18	Sequence 18, Appl
22	82.5	8.9	224	US-09-270-767-43554	Sequence 43554, A
23	82.5	8.9	279	US-09-248-756A-16033	Sequence 16033, A
24	82	8.8	395	US-09-560-761-22	Sequence 22, Appli
25	81.5	8.8	388	US-08-087-772A-2	Sequence 2, Appli
26	81.5	8.8	400	US-08-351-473B-5	Sequence 5, Appli
27	81.5	8.8	400	US-08-450-962-4	Sequence 4, Appli

28	81.5	8.8	400	3	US-08-450-962-6	Sequence 6, Appli
29	81.5	8.8	400	4	US-08-848-631-4	Sequence 4, Appli
30	81.5	8.8	400	4	US-08-848-631-6	Sequence 6, Appli
31	81	8.7	255	4	US-09-549-848B-24	Sequence 24, Appli
32	81	8.7	257	4	US-09-560-761-12	Sequence 12, Appli
33	81	8.7	304	3	US-09-134-001C-4518	Sequence 4518, Ap
34	81	8.7	382	4	US-09-560-761-14	Sequence 14, Appli
35	80.5	8.7	262	3	US-09-134-001C-3932	Sequence 3932, Ap
36	80.5	8.7	430	4	US-09-489-039A-10587	Sequence 10587, A
37	80	8.6	597	4	US-09-252-991A-32657	Sequence 32657, A
38	79	8.5	373	4	US-09-107-532A-6084	Sequence 6084, Ap
39	78.5	8.4	383	4	US-09-560-761-28	Sequence 28, Appli
40	78.5	8.4	408	3	US-09-134-001C-3410	Sequence 3410, Ap
41	78	8.4	263	4	US-10-000-489-40	Sequence 40, Appli
42	78	8.4	957	4	US-09-489-039A-11233	Sequence 11233, A
43	77.5	8.3	255	4	US-09-328-352-7902	Sequence 7902, Ap
44	77.5	8.3	344	4	US-09-252-991A-31786	Sequence 31786, A
45	77.5	8.3	345	4	US-09-107-532A-4426	Sequence 4426, Ap

ALIGNMENTS

RESULT 1
US-08-695-736-3
; Sequence 3, Application US/09695736
; Patent No. 5843714
; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice
; APPLICANT: Bandman, Olga
; APPLICANT: Goli, Surya K.
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: NOVEL HUMAN PROTEOLIPID
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/695,736
; FILING DATE: Filed Herewith
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/POCKET NUMBER: PF-0108 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 157 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 1346732
US-08-695-736-3

Query Match 79.7%; Score 741; DB 2; Length 157;
Best Local Similarity 87.9%; Pred No. 4, 9e-72;
Matches 138; Conservative 13; Mismatches 6; Indels 0; Gaps 0;
QY 26 LRPDJGVRSGALMLLQVLGLVWALADTPHYLYPAIGWVFAVFLWLVTLVFN 85

Db 1 MRPDGLFVRSALGVALLQLVLGLVWALIADTPYHLYPAYGWMVFVAVFLMLVTVFFI 60
QY 86 LYLFLQHLKLMVWPLVLMFNISATVLYITAFIACSAVDLTSLRGTPYQNRASAF 145
Db 61 IYLFQHLKLMVWPLVLLVFFVAAATVLYITAFVACAAAVDLTSLRGSRPYNQRAASF 120
QY 146 FACLVMIAYGVSFFSQNRGVSNAATSQMAGGYA 182
Db 121 FACLVMIAYGVSFFSQNRGVSNAATSQMAGGYS 157

RESULT 2
US-08-695-736-1
; Sequence 1, Application US/08695736
; Patent No. 5843714
; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice
; APPLICANT: Bandman, Olga
; APPLICANT: Goli, Surya K.
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: NOVEL HUMAN PROTEOLIPID
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; FILING DATE: Filed Herewith
; APPLICATION NUMBER: US/08/695,736
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0108 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 153 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: BRSTNOT03
; CLONE: 640699

US-08-695-736-1
Query Match 33.0%; Score 307; DB 2; Length 153;
Best Local Similarity 44.6%; Pred. No. 2.2e-25;
Matches 66; Conservative 27; Mismatches 47; Indels 8; Gaps 2;
QY 22 SVSALRPDLGFRVSRIGALMLQLVLGLVWALIADTPYHLYPAYGWMVFVAVFLVLI 81
Db 6 SSSSFAYDREFLTLPGFLVIAEIVLGLVWALIAGTEYFVPAFGWMVFVAVFLVLI 65
QY 82 VLFLNLYLPOLHMKLMVWPLVLMFNISATVLYITAFIACSAVDLTSL---RGTRPYN 138
Db 66 FELIYITWTYTRIQVPMPTTVGLCFNGSAFVLYLSA-----AVVDASSVSPDRDSHFN 120
QY 139 QRAAASFFACLVMIAYGVSFFSQNR 166
Db 121 SWAASSFFAFVLCVAGNTYFSPFAWR 148

RESULT 3
US-08-695-736-4
; Sequence 4, Application US/08695736
; Patent No. 5843714
; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice
; APPLICANT: Bandman, Olga
; APPLICANT: Goli, Surya K.
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: NOVEL HUMAN PROTEOLIPID
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; FILING DATE: Filed Herewith
; APPLICATION NUMBER: US/08/695,736
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0108 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 153 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 126719
US-08-695-736-4
Query Match 16.5%; Score 153; DB 2; Length 153;
Best Local Similarity 30.2%; Pred. No. 7.8e-09;
Matches 45; Conservative 25; Mismatches 61; Indels 18; Gaps 6;

QY 22 SVSALRPDLGFRVSRIGALMLQLVLGLVWALIADTPYHLYPAYGWMVFVAVFLVLI 79
Db 17 SVFTTLPLD-----LFIFFIFGGLVWILVASSLVFWPL--VQGWVWFVSVECFVA 65
QY 80 TIVFLNLYLPOLHMKLMVWPLVLMFNISATVLYITAFIACSAVDLTSLRG--TRPY 137
Db 66 TTVLILYIIGAHGG--ETSWVLDAAYHCTALFYLSASV-LEALATITMQDGFYRY 122
QY 138 NQRAAASFFACLVMIAYGVSFFSQNR 166
Db 123 HENIAAVFSYIATLLYVWHAVERLIRWK 151

RESULT 4
US-09-702-705-338
; Sequence 338, Application US/09702705
; Patent No. 6504010
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom

[illegible]

	QY	157 SAFFSY 162 Db	141 HAFSIY 146
RESULT 6			
US-09-614-124B-338			
; Sequence 338, Application US/09614124B			
; Patent No. 6630574			
; GENERAL INFORMATION:			
; APPLICANT: Wang, Tongtong			
; APPLICANT: Bangur, Chaitanya S.			
; APPLICANT: Lodes, Michael A.			
; APPLICANT: Fanger, Gary			
; APPLICANT: Vedvick, Tom			
; APPLICANT: Carter, Darrick			
; APPLICANT: Retter, Marc			
; APPLICANT: Mannion, Jane			
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND			
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER			
; FILE REFERENCE: 210121.478C9			
; CURRENT APPLICATION NUMBER: US/09/614,124B			
; CURRENT FILING DATE: 2001-07-11			
; NUMBER OF SEQ ID NOS: 1668			
; SOFTWARE: FastSeq for Windows Version 3.0			
; SEQ ID NO 338			
; LENGTH: 148			
; TYPE: PRT			
; ORGANISM: Homo sapiens			
US-09-614-124B-338			
Query Match 16.0%; Score 148.5; DB 4; Length 148;			
Best Local Similarity 30.2%; Pred.No. 2.3e-08;			
Matches 38; Conservative 31; Mismatches 52; Indels 5; Gaps 4;			
	QY	39 ALMLQLVLGLVWALIADTPHYLYP-AYGWMVFVAFLWLVTIVLFNLFLFQLHMKLYM 97	
	DB	24 AFPLPELIFGFLWTMTAAAT-HIYPPLQGVMYVSLSFSLMFLLSYSILFGFYKR--F 80	
	QY	98 VPMPLVLMFNISATVLIYT-AFIACSAADVLTSLRGTRPNQRQAASFFACLVMIA YGV 156	
	DB	81 ESNRVLDLSYHGTTGLYSMAAVLVQHATTIVEKLPDRIYYINSAASFPAFIATLLYL 140	
	QY	157 SAFFSY 162	
	DB	141 HAFSIY 146	
RESULT 7			
US-09-671-325-338			
; Sequence 338, Application US/09671325			
; Patent No. 6667154			
; GENERAL INFORMATION:			
; APPLICANT: Wang, Tongtong			
; APPLICANT: Bangur, Chaitanya S.			
; APPLICANT: Lodes, Michael A.			
; APPLICANT: Fanger, Gary			
; APPLICANT: Vedvick, Tom			
; APPLICANT: Carter, Darrick			
; APPLICANT: Retter, Marc			
; APPLICANT: Mannion, Jane			
; APPLICANT: Fan, Liqun			
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND			
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER			
; FILE REFERENCE: 210121.478C12			
; CURRENT APPLICATION NUMBER: US/09/671,325			
; CURRENT FILING DATE: 2000-09-26			
; NUMBER OF SEQ ID NOS: 1825			
; SOFTWARE: FastSeq for Windows Version 3.0			
; SEQ ID NO 338			
; LENGTH: 148			
; TYPE: PRT			
US-09-702-703-338			
Query Match 16.0%; Score 148.5; DB 4; Length 148;			
Best Local Similarity 30.2%; Pred.No. 2.3e-08;			
Matches 38; Conservative 31; Mismatches 52; Indels 5; Gaps 4;			
	QY	39 ALMLQLVLGLVWALIADTPHYLYP-AYGWMVFVAFLWLVTIVLFNLFLFQLHMKLYM 97	
	DB	24 AFPLPELIFGFLWTMTAAAT-HIYPPLQGVMYVSLSFSLMFLLSYSILFGFYKR--F 80	
	QY	98 VPMPVLMFNISATVLIYT-AFIACSAADVLTSLRGTRPNQRQAASFFACLVMIA YGV 156	
	DB	81 ESNRVLDLSYHGTTGLYSMAAVLVQHATTIVEKLPDRIYYINSAASFPAFIATLLYL 140	
	QY	157 SAFFSY 162	
	DB	141 HAFSIY 146	
RESULT 5			
US-09-736-457-338			
; Sequence 338, Application US/09736457			
; Patent No. 6509448			
; GENERAL INFORMATION:			
; APPLICANT: Wang, Tongtong			
; APPLICANT: Bangur, Chaitanya S.			
; APPLICANT: Lodes, Michael A.			
; APPLICANT: Fanger, Gary			
; APPLICANT: Vedvick, Tom			
; APPLICANT: Carter, Darrick			
; APPLICANT: Retter, Marc			
; APPLICANT: Mannion, Jane			
; APPLICANT: Fan, Liqun			
; APPLICANT: Wang, Aljun			
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND			
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER			
; FILE REFERENCE: 210121.478C15			
; CURRENT APPLICATION NUMBER: US/09/736,457			
; CURRENT FILING DATE: 2000-12-13			
; NUMBER OF SEQ ID NOS: 1864			
; SOFTWARE: FastSeq for Windows Version 3.0			
; SEQ ID NO 338			
; LENGTH: 148			
; TYPE: PRT			
; ORGANISM: Homo sapiens			
US-09-736-457-338			
Query Match 16.0%; Score 148.5; DB 4; Length 148;			
Best Local Similarity 30.2%; Pred.No. 2.3e-08;			
Matches 38; Conservative 31; Mismatches 52; Indels 5; Gaps 4;			
	QY	39 ALMLQLVLGLVWALIADTPHYLYP-AYGWMVFVAFLWLVTIVLFNLFLFQLHMKLYM 97	
	DB	24 AFPLPELIFGFLWTMTAAAT-HIYPPLQGVMYVSLSFSLMFLLSYSILFGFYKR--F 80	
	QY	98 VPMPLVLMFNISATVLIYT-AFIACSAADVLTSLRGTRPNQRQAASFFACLVMIA YGV 156	
	DB	81 ESNRVLDLSYHGTTGLYSMAAVLVQHATTIVEKLPDRIYYINSAASFPAFIATLLYL 140	

[illegible]

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; ORGANISM: Homo sapiens
US-09-671-325-338

Query Match      16.0%; Score 148.5; DB 4; Length 148;
Best Local Similarity 30.2%; Pred. No. 2.3e-08;
Matches 38; Conservative 31; Mismatches 52; Indels 5; Gaps 4;

QY 39 ALMLQLVLGLLWALIADTPHYLYP-AYGWMFVAVFLWLVTLVFNLYLFQHLHMKLYM 97
Db 24 AFFLPELIFGLVMTWVAAT-HIVYPLQGWVMYVSLTSLMLFLLSYLFGFYKR--F 80
QY 98 VPWPLVMIFNISATVLYIT-AFIACSAAVDLTSLRGTRPNQRAAASFFACLVMYAGV 156
Db 81 ESMRVLDSLYHGTTGLYMSAAVLQVHATIVSEKLLDPRIYYINSAASFFAFIATLLYL 140
QY 157 SAFPSY 162
Db 141 HAFSIY 146

RESULT 8
US-09-589-184-338
; Sequence 338, Application US/09589184
; Patent No. 6686447
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; FILE REFERENCE: 210121.478C8
; CURRENT APPLICATION NUMBER: US/09/589,184
; CURRENT FILING DATE: 2000-06-05
; NUMBER OF SEQ ID NOS: 827
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 338
; LENGTH: 148
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-589-184-338

Query Match      16.0%; Score 148.5; DB 4; Length 148;
Best Local Similarity 30.2%; Pred. No. 2.3e-08;
Matches 38; Conservative 31; Mismatches 52; Indels 5; Gaps 4;

QY 39 ALMLQLVLGLLWALIADTPHYLYP-AYGWMFVAVFLWLVTLVFNLYLFQHLHMKLYM 97
Db 24 AFFLPELIFGLVMTWVAAT-HIVYPLQGWVMYVSLTSLMLFLLSYLFGFYKR--F 80
QY 98 VPWPLVMIFNISATVLYIT-AFIACSAAVDLTSLRGTRPNQRAAASFFACLVMYAGV 156
Db 81 ESMRVLDSLYHGTTGLYMSAAVLQVHATIVSEKLLDPRIYYINSAASFFAFIATLLYL 140
QY 157 SAFPSY 162
Db 141 HAFSIY 146

RESULT 9
US-09-658-824-338
; Sequence 338, Application US/09658824
; Patent No. 6746846
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
```

```
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; FILE REFERENCE: 210121.478C11
; CURRENT APPLICATION NUMBER: US/09/658,824
; CURRENT FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 1788
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 338
; LENGTH: 148
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-658-824-338

Query Match      16.0%; Score 148.5; DB 4; Length 148;
Best Local Similarity 30.2%; Pred. No. 2.3e-08;
Matches 38; Conservative 31; Mismatches 52; Indels 5; Gaps 4;

QY 39 ALMLQLVLGLLWALIADTPHYLYP-AYGWMFVAVFLWLVTLVFNLYLFQHLHMKLYM 97
Db 24 AFFLPELIFGLVMTWVAAT-HIVYPLQGWVMYVSLTSLMLFLLSYLFGFYKR--F 80
QY 98 VPWPLVMIFNISATVLYIT-AFIACSAAVDLTSLRGTRPNQRAAASFFACLVMYAGV 156
Db 81 ESMRVLDSLYHGTTGLYMSAAVLQVHATIVSEKLLDPRIYYINSAASFFAFIATLLYL 140
QY 157 SAFPSY 162
Db 141 HAFSIY 146

RESULT 10
US-09-520-781-28
; Sequence 28, Application US/09520781
; Patent No. 6689866
; GENERAL INFORMATION:
; APPLICANT: Shinkets, Richard A.
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES AND PROTEINS ENCODED THEREBY
; FILE REFERENCE: 15966-540 No. 6689866el Polynucleotides
; CURRENT APPLICATION NUMBER: US/09/520,781
; CURRENT FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: USSN 60/123,667
; PRIOR FILING DATE: 1999-03-09
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 28
; LENGTH: 299
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-520-781-28

Query Match      13.7%; Score 127.5; DB 4; Length 299;
Best Local Similarity 25.7%; Pred. No. 9.9e-06;
Matches 38; Conservative 25; Mismatches 66; Indels 19; Gaps 3;

QY 37 LGALMLQLVLGLLWALIADTPHYLYPAYGWMFVAVFLWLVTLVFNLYL-----EQ 90
Db 13 LGLRLQLVSTCTVAFSLVASVGAWTGSNGNSMTWCFCFSVTLIIILIVELCGLQARFP 72
QY 91 LHMKLYMPWPLVLMIFNISATVLYITAFIACSAAVDLTSLRGTRPNQRAAASFFACL 150
Db 73 LSWRNPFTTACVAALFCLISASIIYPTTV-----QFLSHGRSRDHAIATPFSCIA 124
QY 151 MIAYGVSAFFSYQAWRGVGSNAATSQMA 178
Db 125 CVAYATEV-----AWTRARPGEITGYMA 147

RESULT 11
US-09-198-452A-932
```

```
; Sequence 932, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Grifais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 932
; LENGTH: 421
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-932

Query Match          9.8%; Score 91; DB 4; Length 421;
Best Local Similarity 24.0%; Pred. No. 0.13;
Matches 35; Conservative 24; Mismatches 49; Indels 38; Gaps 5;

QY 23 VSALRDLGFRSLGAL-----MLQLVLGLLVWALIADTPYHLYPAYGVMFVAVFL 76
DB 71 ISSMDPTAMLVTSKGLLNKIMQLRHPALGWVFFICAYDYHLFKRWAVLY--PFM 128
QY 77 MLVTIVFLNLYLFQLHMKLYMVPW-----PLVLMFNISATVLYITAFIACSA 125
DB 129 ICALVGLFFVPSONVHRWYRIFPHMSVQPSYEGKLVIV-----MLSYILES 179
QY 126 VLTSLRGTRPNQRAAASFFACLVM 151
DB 180 ADITS-----KTTAFLACLVM 195

RESULT 12
US-09-328-714A-4
; Sequence 4, Application US/09328714A
; Patent No. 6500940
; GENERAL INFORMATION:
; APPLICANT: The Salk Institute for Biological Sciences
; APPLICANT: Inder M. Verma
; APPLICANT: Mark Schmitt
; APPLICANT: Nikunj V. Somia
; TITLE OF INVENTION: LIFE GUARD (LFG) POLYNUCLEOTIDES AND
; TITLE OF INVENTION: POLYPEPTIDES AND METHODS OF USE THEREOF
; FILE REFERENCE: SALKINS.016A
; CURRENT APPLICATION NUMBER: US/09/328,714A
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 220
; TYPE: PRT
; ORGANISM: C. elegans
US-09-328-714A-4

Query Match          9.5%; Score 88.5; DB 4; Length 220;
Best Local Similarity 17.7%; Pred. No. 0.11;
Matches 22; Conservative 27; Mismatches 54; Indels 21; Gaps 2;

QY 68 WYMFVAVFLMLTVILF-----NLVLFQLHMKLYMVPWPLVLMFNISATVLY 115
DB 44 WYFIALIVFLVAILSCGNLRQFPVNIILLTIFLSAAVMTFVTACYNVQSVLIC 103
QY 116 ITAFIACSAVDLTSLRGTRPNQRAAASFFACLVMYGVSAF-----FSQAWR 166
DB 104 LCITTCGSGVIFISMKTKSDLTSLRGTRPNQRAAASFFACLVMYGVSAF-----FSQAWR 166
QY 167 GVGS 170
DB 164 GLAA 167

; Sequence 932, Application US/09107532A
; Patent No. 658275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; TITLE OF INVENTION: ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: PC
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 6356:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 296 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Enterococcus faecium
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...296
; SEQUENCE DESCRIPTION: SEQ ID NO: 6356:
US-09-107-532A-6356

Query Match          9.5%; Score 88; DB 4; Length 296;
Best Local Similarity 22.9%; Pred. No. 0.17;
Matches 38; Conservative 26; Mismatches 50; Indels 50; Gaps 7;

QY 46 VLGLVWALIADTPYHL--YPAYGVMFVAVFLMLTVIL-----FNL 86
DB 21 IVGLVVLALVGLFFPYLGMQAKVWALFSLIFLILLLSSATVWSPNQAKVILFPGQ 80
QY 87 YLFQLHMKLYMVPWPLV-----LMFNISATVLYITAFIACSAVDLTSLRGTRPNQ 140
DB 81 YLGTIRENGFFLTPLAQKMTVSLKVRNFNSVLKVN-----BLDG-----NP 127
QY 141 AAAGSF-----FACLVMTAYGVSAFFSQAAMRGVGSNAATSQMAGGY 181
DB 128 AVVFKVVDTKALFDVAY-----YQDFVEIQSETAIRHIAQY 166

; Sequence 328-352-5694
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: US/09328352
; Sequence 5694, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
```

; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 5694
; LENGTH: 448
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-5694

Query Match 9.4%; Score 87; DB 4; Length 448;
Best Local Similarity 22.2%; Pred. No. 0.37; 58; Indels 66; Gaps 7;
Matches 43; Conservative 27; Mismatches 58; Indels 66; Gaps 7;
QY 27 RPDL-----GFVSRRLGALM-----LLQLVLGLLWALIA-----DTPYH----- 61
DQ 69 RPDLGGGYNVAREGFDLIGCSAWGWLCTTIGIVGVYVIAFSGVGMETDSKDHVIFG 128
QY 62 ----LYPAYGWMVAVFLMLV-----TIVLFNLYLF 89
DQ 129 EGNLTLYSLIGSIFWVLVHVLVSRGKEAAIVNLLATIAKIIIMVVFIFFTFIARFDLF 188
QY 90 QLHMKLYWVWPLVIMFNISATVLYITAFIACSAVDLTSLRGTTPYNORA-----A 142
DQ 189 KLNLDLSLKVPLWQVKDMLTLTV--FTGIEGAVLSSRAKNRHDIGKATILGVLLA 246
QY 143 ASPFACLVMIAYGV 156
DQ 247 LSFYVMVTVLAYGV 260

RESULT 15
US-09-252-991A-23822
; Sequence 23822, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 23822
; LENGTH: 211
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23822

Query Match 9.3%; Score 86.5; DB 4; Length 211;
Best Local Similarity 32.8%; Pred. No. 0.16;
Matches 38; Conservative 15; Mismatches 36; Indels 27; Gaps 5;
QY 20 EASVSALRPDLGFV---RSLGALMLLQVLGLVWALIAADTPYHLYPAYGWMFVAV-- 74
DQ 33 QAWIFALGPDGKTYLVDRLGLGALVLLLTLM-----TP--LQKLSGWPQIAVER 82
QY 75 --FLWLVTVLFNLYLF-----QLHMKLYWVWPLVIMFNISATVLYITA 118
DQ 83 QLGLWCFTYVLLHLSAYCVFILGLDWGLGIELSKRPIIIVGMLGFIPLFLAITS 138

Search completed: December 1, 2004, 15:47:42
Job time : 42 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 1, 2004, 15:47:12 ; Search time 145 Seconds
(without alignments)
447.623 Million cell updates/sec

Title: US-09-602-597A-4
Perfect score: 930
Sequence: 1 MAEPFSKVTSTSSPAQAE.....QAWRGVGSNAATSQMAGYA 182

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1582122 seqs, 35623098 residues

Total number of hits satisfying chosen parameters: 1582122

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	930	100.0	216	14	US-10-263-230A-4
2	625	67.2	125	15	US-10-264-237-2440
3	580	62.4	113	15	US-10-264-237-2486
4	325	34.9	173	9	US-09-765-205-44
5	322	34.6	173	15	US-10-296-115-1314
6	283	30.4	132	15	US-10-264-048-2227
7	191	20.5	100	15	US-10-553-593-194
8	191	20.5	101	10	US-09-397-945-194
9	162	17.4	176	11	US-09-833-243-1314
10	162	17.4	176	14	US-10-176-847-20
11	162	17.4	176	14	US-10-097-340-282
12	162	17.4	215	15	US-10-264-049-2873
13	153	16.5	153	14	US-10-257-021-74

chld

14	153	16.5	153	15	US-10-336-603A-22	Sequence 22, Appl
15	148.5	16.0	148	9	US-09-736-457-338	Sequence 338, App
16	148.5	16.0	148	9	US-09-902-941-338	Sequence 338, App
17	148.5	16.0	148	9	US-09-849-626-338	Sequence 338, App
18	148.5	16.0	148	10	US-09-476-300-338	Sequence 338, App
19	148.5	16.0	148	14	US-10-017-754-338	Sequence 338, App
20	148.5	16.0	148	14	US-10-113-872-338	Sequence 338, App
21	148.5	16.0	148	14	US-10-283-017-338	Sequence 338, App
22	148.5	16.0	148	9	US-09-925-300-1297	Sequence 1297, App
23	147.5	15.9	265	14	US-10-103-196-14	Sequence 14, Appl
24	143	15.4	206	14	US-10-106-698-6320	Sequence 6320, App
25	137.5	14.8	322	9	US-09-966-546-20	Sequence 20, Appl
26	137.5	14.8	322	9	US-09-966-545-20	Sequence 20, Appl
27	137.5	14.8	322	10	US-09-965-212-20	Sequence 21, Appl
28	137.5	14.8	322	10	US-09-946-374-31	Sequence 31, Appl
29	137.5	14.8	322	13	US-10-052-586-172	Sequence 172, App
30	137.5	14.8	322	14	US-10-174-590-172	Sequence 172, App
31	137.5	14.8	322	14	US-10-176-758-172	Sequence 172, App
32	137.5	14.8	322	14	US-10-175-737-172	Sequence 172, App
33	137.5	14.8	322	14	US-10-174-581-172	Sequence 172, App
34	137.5	14.8	322	14	US-10-176-483-172	Sequence 172, App
35	137.5	14.8	322	14	US-10-176-749-172	Sequence 172, App
36	137.5	14.8	322	14	US-10-176-914-172	Sequence 172, App
37	137.5	14.8	322	14	US-10-176-915-172	Sequence 172, App
38	137.5	14.8	322	14	US-10-173-706-172	Sequence 172, App
39	137.5	14.8	322	14	US-10-175-738-172	Sequence 172, App
40	137.5	14.8	322	14	US-10-175-752-172	Sequence 172, App
41	137.5	14.8	322	14	US-10-176-482-172	Sequence 172, App
42	137.5	14.8	322	14	US-10-176-757-172	Sequence 172, App
43	137.5	14.8	322	14	US-10-176-913-172	Sequence 172, App
44	137.5	14.8	322	14	US-10-180-552-172	Sequence 172, App
45	137.5	14.8	322	14	US-10-180-557-172	Sequence 172, App

ALIGNMENTS

RESULT 1

US-10-263-230A-4
; Sequence 4, Application US/10263230A
; Publication No. US20030152963A1
; GENERAL INFORMATION:
; APPLICANT: Duhi, David
; APPLICANT: Gorman, Susan Wilkie
; TITLE OF INVENTION: HUMAN CHROMOSOME 15 AND 16 BARDET-BIEDL
; SYNDROME POLYNUCLEOTIDES AND POLYPEPTIDES AND METHODS OF USE
; FILE REFERENCE: 59516-243/PP-1568.002
; CURRENT APPLICATION NUMBER: US/10/263.230A
; CURRENT FILING DATE: 2002-10-02
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 216
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-263-230A-4

Query Match	100.0%	Score	930	DB	14	Length	216
Best Local Similarity	100.0%	Pred. No.	5.4e-88				
Matches	182	Conservative	0	Mismatches	0	Indels	0
Gaps	0						
QY	1	MAEPFSKVTSTSSPAQAEASVSALRDLGFSVSRGALMLQLVLGLLYWALIADTPY	60				
Db	1	MAEPFSKVTSTSSPAQAEASVSALRDLGFSVSRGALMLQLVLGLLYWALIADTPY	60				
QY	61	HLYPAGWVMFVAVFLWLTVTLVFNLYLFQHLMKLYMVPWPLVLMIFNISATVLYITAFI	120				
Db	61	HLYPAGWVMFVAVFLWLTVTLVFNLYLFQHLMKLYMVPWPLVLMIFNISATVLYITAFI	120				
QY	121	ACSAAVDITSLRGTPYNNORAAASFPACLVMIAYGVSAFFSYQAWRGVGSNAATSQMAGG	180				
Db	121	ACSAAVDITSLRGTPYNNORAAASFPACLVMIAYGVSAFFSYQAWRGVGSNAATSQMAGG	180				

QY 181 YA 182
 Db 181 YA 182

RESULT 2
 US-10-264-237-2440
 ; Sequence 2440, Application US/10264237
 ; Publication No. US20040009491A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Birse et al.
 ; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
 ; FILE REFERENCE: P131P1
 ; CURRENT APPLICATION NUMBER: US/10/264,237
 ; CURRENT FILING DATE: 2002-10-04
 ; PRIOR APPLICATION NUMBER: PCT/US01/16450
 ; PRIOR FILING DATE: 2001-05-18
 ; PRIOR APPLICATION NUMBER: US 60/205,515
 ; PRIOR FILING DATE: 2000-05-19
 ; NUMBER OF SEQ ID NOS: 2876
 ; SOFTWARE: Patent in Ver. 3.1
 ; SEQ ID NO 2440
 ; LENGTH: 125
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; NAME/KEY: MISC_FEATURE
 ; LOCATION: (118)
 ; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
 US-10-264-237-2440

Query Match 67.2%; Score 625; DB 15; Length 125;
 Best Local Similarity 97.6%; Pred. No. 1e-56; Indels 0; Gaps 0;
 Matches 122; Conservative 0; Mismatches 3;

QY 1 MAEPSPKSVTRTSSPAQGAASVSALRPDLGFRVSRIGALMLQLVLGLLVWALIADTPY 60
 Db 1 MAEPSPKSVTRTSSPAQGAASVSALRPDLGFRVSRIGALMLQLVLGLLVWALIADTPY 60

QY 61 HLPAYGVWVAVFLMLVTLVFNLYLQHLHMKLYMVPWPLVLMFNISATVLYITATP 120
 Db 61 HLPAYGVWVAVFLMLVTLVFNLYLQHLHMKLYMVPWPLVLMFNISATVLYITATP 120

QY 121 ACSAA 125
 Db 121 GCSAA 125

RESULT 3
 US-10-264-237-2486
 ; Sequence 2486, Application US/10264237
 ; Publication No. US20040009491A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Birse et al.
 ; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
 ; FILE REFERENCE: P131P1
 ; CURRENT APPLICATION NUMBER: US/10/264,237
 ; CURRENT FILING DATE: 2002-10-04
 ; PRIOR APPLICATION NUMBER: PCT/US01/16450
 ; PRIOR FILING DATE: 2001-05-18
 ; PRIOR APPLICATION NUMBER: US 60/205,515
 ; PRIOR FILING DATE: 2000-05-19
 ; NUMBER OF SEQ ID NOS: 2876
 ; SOFTWARE: Patent in Ver. 3.1
 ; SEQ ID NO 2486
 ; LENGTH: 113
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-264-237-2486

Query Match 62.4%; Score 580; DB 15; Length 113;
 Best Local Similarity 100.0%; Pred. No. 4.2e-52; Indels 0; Gaps 0;
 Matches 113; Conservative 0; Mismatches 0;

QY 70 MFVAVFLMLVTLVFNLYLQHLHMKLYMVPWPLVLMFNISATVLYITAFIACSAAVDLT 129
 Db 1 MFVAVFLMLVTLVFNLYLQHLHMKLYMVPWPLVLMFNISATVLYITAFIACSAAVDLT 60

QY 130 SLRGTRPNQRAAASFFACLVMIAYGVSAFFSYQAWRGVGSNAATSONAGGYA 182
 Db 61 SLRGTRPNQRAAASFFACLVMIAYGVSAFFSYQAWRGVGSNAATSONAGGYA 113

RESULT 4
 US-09-765-205-44
 ; Sequence 44, Application US/09765205
 ; Patent No. US20020034800A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Cao, Li
 ; TITLE OF INVENTION: BONE MARROW SECRETED PROTEINS AND POLYNUCLEOTIDES
 ; FILE REFERENCE: 1458.004/200130.449
 ; CURRENT APPLICATION NUMBER: US/09/765,205
 ; CURRENT FILING DATE: 2001-01-17
 ; PRIOR APPLICATION NUMBER: US/09/212,440
 ; PRIOR FILING DATE: 1998-12-16
 ; NUMBER OF SEQ ID NOS: 46
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 44
 ; LENGTH: 173
 ; TYPE: PRT
 ; ORGANISM: human
 US-09-765-205-44

Query Match 34.9%; Score 325; DB 9; Length 173;
 Best Local Similarity 43.8%; Pred. No. 1.7e-25; Indels 8; Gaps 2;
 Matches 71; Conservative 29; Mismatches 54;

QY 8 VSTRTSSPAQGAASVSALRPDLGFRVSRIGALMLQLVLGLLVWALIADTPYHLYPAG 67
 Db 12 VTTASSGFAENFSSSSSFAYDREFRLTLPGLFLIVAVILGLLWTLIAGTEYFRVPAFG 71

QY 68 WMFVAVFLMLVTLVFNLYLQHLHMKLYMVPWPLVLMFNISATVLYITAFIACSAAVD 127
 Db 72 WMFVAVFLMLVTLVFNLYLQHLHMKLYMVPWPLVLMFNISATVLYITAFIACSAAVD 125

QY 128 LTSL---RGTRPNQRAAASFFACLVMIAYGVSAFFSYQAWR 166
 Db 127 ASSVSPEDSHNFNSWAASSFFFLVITICAGNTYFSAIWR 168

RESULT 5
 US-10-296-115-1314
 ; Sequence 1314, Application US/10296115
 ; Publication No. US20040053248A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hyseq Inc
 ; TITLE OF INVENTION: No. US20040053248A1e1 Nucleic Acids and Polypeptides
 ; FILE REFERENCE: 784PCT
 ; CURRENT APPLICATION NUMBER: US/10/296,115
 ; CURRENT FILING DATE: 2002-11-18
 ; PRIOR APPLICATION NUMBER: US09/488,725
 ; PRIOR FILING DATE: 2000-01-21
 ; PRIOR APPLICATION NUMBER: US09/552,317
 ; PRIOR FILING DATE: 2000-04-25
 ; NUMBER OF SEQ ID NOS: 1478
 ; SEQ ID NO 1314
 ; LENGTH: 173
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-296-115-1314

Query Match 34.6%; Score 322; DB 15; Length 173;
 Best Local Similarity 42.4%; Pred. No. 3.4e-25; Indels 8; Gaps 2;
 Matches 70; Conservative 30; Mismatches 57;

QY 5 PSKVSTRTSSPAQGAASVSALRPDLGFRVSRIGALMLQLVLGLLVWALIADTPYHLYP 64

Db 9 PNACTRYKVPALSVHTSSSFAYDREFLTLFGFLVAEIVGLLVWTLIAGTEVRVP 68
QY 55 AYGNMFVAVFLMLVTLVFNLYLQHLMKLYMVPWPLVMFNISATVLYITAFIACA 124
Db 69 AFGNMFVAVFWLTVFFLIITMTYTRIPQVPWTTVGLCFNGSAFVLYLSA-----A 123
QY 125 AVDLTSL---RGRTPYNORAAAFACLVMIAYGVSAFTSYQAWR 166
Db 124 VVDASSVSPERDSHNFNSWAASSFFAFPLVTICVAGNTYFSFIAR 168

RESULT 6

US-10-264-049-2227
; Sequence 2227, Application US/10264049
; Publication No. US20040005579A1
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: P4133P1
; CURRENT APPLICATION NUMBER: US/10/264,049
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/18569
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: US 60/209,467
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 4360
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 2227
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-264-049-2227

Query Match 30.4%; Score 283; DB 15; Length 132;

Best Local Similarity 46.0%; Pred. No. 2.7e-21;

Matches 58; Conservative 23; Mismatches 37; Indels 8; Gaps 2;

QY 44 QLVGLLVWALIDTPYHLYPAYGWMFVAVFLVLTIVFLNLYLQHLMKLYMVPWPLV 103
Db 7 EIVGLLVWTLIAGTEVRYPAGGWMFVAVFWLTVFLLIYITMTYTRIPQVPWTV 66
QY 104 LMFINISATVLYITAFIACSAVDLTSL---RGRTPYNORAAAFACLVMIAYGVSAFP 160
Db 67 GLCFNGSAFVLYLSA-----AVVDASSVSPKDSHNFNSWAASSFFAFPLVTICVAGNTYF 121
QY 161 SYQAWR 166
Db 122 SFIAR 127

RESULT 7

US-10-653-595-194
; Sequence 194, Application US/10653595
; Publication No. US20040048304A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et. al.
; TITLE OF INVENTION: 95 Human secreted proteins
; FILE REFERENCE: P2027P1C1
; CURRENT APPLICATION NUMBER: US/10/653,595
; CURRENT FILING DATE: 2003-09-03
; PRIOR APPLICATION NUMBER: US 09/397945
; PRIOR FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: PCT/US99/05804
; PRIOR FILING DATE: 1999-03-18
; PRIOR APPLICATION NUMBER: 60/078,566
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/078,576
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/078,573
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/078,563
; PRIOR FILING DATE: 1998-03-19

; PRIOR APPLICATION NUMBER: 60/078,579
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/080,314
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/080,312
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/078,578
; PRIOR FILING DATE: 1998-03-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 470
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 194
; LENGTH: 100
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (92)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (96)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-653-595-194

Query Match 20.5%; Score 191; DB 15; Length 100;

Best Local Similarity 41.0%; Pred. No. 6.5e-12;

Matches 41; Conservative 20; Mismatches 31; Indels 8; Gaps 2;

QY 70 MFVAVFLVLTIVFLNLYLQHLMKLYMVPWPLVMFNISATVLYITAFIACSAVDLT 129
Db 1 MFVAVFWLTVFLLIITMTYTRIPQVPWTTVGLCFNGSAFVLYLSA-----AVVDAS 55
QY 130 SL---RGRTPYNORAAAFACLVMIAYGVSAFFSYQAWR 166
Db 56 SVSPKDSHNFNSWAASSFFAFPLVTICVAGNTYFSFXAWR 95

RESULT 8

US-09-397-945-194
; Sequence 194, Application US/09397945
; Publication No. US200300065139A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc. et al.
; TITLE OF INVENTION: 95 Human secreted proteins
; FILE REFERENCE: P2027P1
; CURRENT APPLICATION NUMBER: US/09/397,945
; CURRENT FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: PCT/US99/05804
; PRIOR FILING DATE: 1999-03-18
; PRIOR APPLICATION NUMBER: 60/078,566
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/078,576
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/078,573
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/078,574
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/078,579
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/080,314
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/080,312
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/078,578
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/078,581
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/078,577
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/078,563
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/080,313

;; PRIOR FILING DATE: 1998-04-01
;; NUMBER OF SEQ ID NOS: 470
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 194
;; LENGTH: 101
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: SITE
;; LOCATION: (92)
;; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
;; NAME/KEY: SITE
;; LOCATION: (96)
;; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
;; NAME/KEY: SITE
;; LOCATION: (101)
;; OTHER INFORMATION: Xaa equals stop translation
US-09-397-945-194

Query Match 20.5%; Score 191; DB 10; Length 101;
Best Local Similarity 41.0%; Pred. No. 6.6e-12;
Matches 41; Conservative 20; Mismatches 31; Indels 8; Gaps 2;
QY 70 MFVAVFLWLVTVLNLVQLHMKLVMPVPLVLMFNISATVLYITAFIACSAVDLT 129
DB 1 MFVAVFWLVTVLNLVQLHMKLVMPVPLVLMFNISATVLYITAFIACSAVDLT 129
QY 130 SL--RGTPTYNQRAAASFFACLVMIAYGVSAFFSYQAWR 166
DB 56 SVSPKDSHNFNGSWAASSPFAFLVTCYAGNTVFSFXWR 95

RESULT 9
US-09-833-245-1314
;; Sequence 1314, Application US/09833245
;; Publication No. US20040010134A1
;; GENERAL INFORMATION:
;; APPLICANT: Human Genome Sciences, Inc.
;; TITLE OF INVENTION: Albumin Fusion Proteins
;; FILE REFERENCE: PF546PCT
;; CURRENT APPLICATION NUMBER: US/09/833,245
;; PRIOR FILING DATE: 2001-04-12
;; PRIOR APPLICATION NUMBER: 60/229,358
;; PRIOR FILING DATE: 2000-04-12
;; PRIOR APPLICATION NUMBER: 60/256,931
;; PRIOR FILING DATE: 2000-12-21
;; PRIOR APPLICATION NUMBER: 60/199,384
;; PRIOR FILING DATE: 2000-04-25
;; NUMBER OF SEQ ID NOS: 2267
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 1314
;; LENGTH: 176
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-833-245-1314

Query Match 17.4%; Score 162; DB 11; Length 176;
Best Local Similarity 28.7%; Pred. No. 1.2e-08;
Matches 43; Conservative 30; Mismatches 63; Indels 14; Gaps 4;
QY 28 PDLGFRSLGALMLQLVLGLLVWALIADTPYHLYPAYGWMFVAVFLWLVTVLNLV 87
DB 29 PDI--LRTYSGAFVCLLEIFGLVWILVASSNVPLPILQGVWVSVTAFFSLLFLGMF 86
QY 88 LPQLHMKLVMPVPLVLMFNISATVLYITAFIACSAVDL-----TSLEG-----TRP 136
DB 87 LSGWVAQI--DANWNFLDFAYHFTVFYFGAFLEAATSLHDLHCNTTITGQPLLSDNQ 145
QY 137 YNQRAAASFFACLVMIAYGVSAFFSYQAWR 166
DB 146 YNINVAASIFAFMTTACYCGLGLALRRWR 175

RESULT 10
US-10-176-847-20
;; Sequence 20, Application US/10176847
;; Publication No. US20030068636A1
;; GENERAL INFORMATION:
;; APPLICANT: Veiby, Pette Ole
;; TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR
;; IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF BREAST
;; TUMORS
;; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF BREAST
;; TUMORS
;; FILE REFERENCE: MRI-039
;; CURRENT APPLICATION NUMBER: US/10/176,847
;; CURRENT FILING DATE: 2002-06-21
;; NUMBER OF SEQ ID NOS: 112
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 20
;; LENGTH: 176
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-176-847-20

Query Match 17.4%; Score 162; DB 14; Length 176;
Best Local Similarity 28.7%; Pred. No. 1.2e-08;
Matches 43; Conservative 30; Mismatches 63; Indels 14; Gaps 4;
QY 28 PDLGFRSLGALMLQLVLGLLVWALIADTPYHLYPAYGWMFVAVFLWLVTVLNLV 87
DB 29 PDI--LRTYSGAFVCLLEIFGLVWILVASSNVPLPILQGVWVSVTAFFSLLFLGMF 86
QY 88 LPQLHMKLVMPVPLVLMFNISATVLYITAFIACSAVDL-----TSLEG-----TRP 136
DB 87 LSGWVAQI--DANWNFLDFAYHFTVFYFGAFLEAATSLHDLHCNTTITGQPLLSDNQ 145
QY 137 YNQRAAASFFACLVMIAYGVSAFFSYQAWR 166
DB 146 YNINVAASIFAFMTTACYCGLGLALRRWR 175

RESULT 11
US-10-097-340-282
;; Sequence 282, Application US/10097340
;; Publication No. US20030087250A1
;; GENERAL INFORMATION:
;; APPLICANT: John MONAHAN
;; APPLICANT: Manjula GANNAVAPURU
;; APPLICANT: Sebastian HOERSCH
;; APPLICANT: Shubhangi KAMATKAR
;; APPLICANT: Steve G. KOVATS
;; APPLICANT: Rachel E. MEYERS
;; APPLICANT: Michael MORRISSEY
;; APPLICANT: Peter OLANDT
;; APPLICANT: Ami SEN
;; APPLICANT: Peter VEIBY
;; APPLICANT: Gordon B. MILLS
;; APPLICANT: Robert C. BAST, Jr.
;; APPLICANT: Karen LU
;; APPLICANT: Rosemarie SCHMANDT
;; APPLICANT: Xumel ZHAO
;; APPLICANT: Karen GLATT
;; TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identification,
;; Prevention, and Therapy of Ovarian Cancer
;; FILE REFERENCE: MRI-030
;; CURRENT APPLICATION NUMBER: US/10/097,340
;; PRIOR FILING DATE: 2002-03-14
;; PRIOR APPLICATION NUMBER: 60/276,025
;; PRIOR FILING DATE: 2001-03-14
;; PRIOR APPLICATION NUMBER: 60/325,149
;; PRIOR FILING DATE: 2001-09-26
;; PRIOR APPLICATION NUMBER: 60/276,026
;; PRIOR FILING DATE: 2001-03-14
;; PRIOR APPLICATION NUMBER: 60/324,967
;; PRIOR FILING DATE: 2001/09/26
;; PRIOR APPLICATION NUMBER: 60/311,732
;; PRIOR FILING DATE: 2001-08-10

Db 123 HENIAAVFSYIATLLVYVHVFSLRWK 151

RESULT 15

US-09-736-457-338
; Sequence 338, Application US/09736457
; Patent No. US20020168637A1

GENERAL INFORMATION:

; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; APPLICANT: Wang, AiJun

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.478C15

; CURRENT APPLICATION NUMBER: US/09/736,457

; CURRENT FILING DATE: 2000-12-13

; NUMBER OF SEQ ID NOS: 1864

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 338

; LENGTH: 148

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-736-457-338

Query Match 16.0%; Score 148.5; DB 9; Length 148;
Best Local Similarity 30.2%; Pred. No. 2.5e-07;
Matches 38; Conservative 31; Mismatches 52; Indels 5; Gaps 4;

QY 39 ALMLQLVGLLVNLIADTPHYLP-AYGWMFVAVFLWLVTLVFNLYLQLHMKLYM 97

Db 24 AFPELIFGLFVMTVAAT-HIVYPLLOGVMWYVSLTSLMFLSLYLFYGR--F 80

QY 98 VPMPLVMIFNISATVLYIT-AFIACSAAVDLTSLRGTPYNGRAAASPFACLVMIAVGV 156

Db 81 ESKRVLDLSLHGTTGILYMSAAVLQVHATVSEKLDLPRIYINSAAFPFAIATLLYL 140

QY 157 SAFFSY 162

Db 141 HAFSIY 146

Search completed: December 1, 2004, 15:59:25
Job time : 147 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 1, 2004, 15:40:54 ; Search time 39 Seconds
(without alignments)
449,012 Million cell updates/sec

Title: US-09-602-597A-4
Perfect score: 930
Sequence: 1 NAEFPSKVSTRTSPAQAE.....QAWRGVGSNAATSQMAGGYA 182

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 79:**

1: Pir1:**

2: Pir2:**

3: Pir3:**

4: Pir4:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	741	79.7	157	2 A55046	plasmolipin - rat
2	158	17.0	281	2 T29464	hypothetical prote
3	153	16.5	153	2 A29472	T-cell surface gly
4	148.5	16.0	148	2 I38891	hypothetical prote
5	145.5	15.6	153	2 S68406	vesicular integral
6	141	15.2	156	2 T29152	hypothetical prote
7	95.5	10.3	242	2 T19564	hypothetical prote
8	95.5	10.3	444	2 I39294	McLeod syndrome-as
9	95	10.2	276	2 S13585	nosy protein precu
10	94.5	10.2	152	2 S32567	A4 protein - human
11	92.5	9.9	401	1 YOECHQ	sodium-glutamate s
12	91.5	9.8	401	2 A98195	glutamate transpor
13	91.5	9.8	401	2 B86042	glutamate transpor
14	91	9.8	208	2 T23328	hypothetical prote
15	91	9.8	379	2 D81515	cell shape-determi
16	91	9.8	415	2 A86399	rod shape protein
17	91	9.8	415	2 C72026	rod shape protein
18	90.5	9.7	404	1 LAB8CA	latent membrane pr
19	90.5	9.7	461	2 G85059	amino acid transpo
20	90	9.7	539	2 D69748	probable sugar tra
21	89.5	9.6	202	2 B83059	hypothetical prote
22	89	9.6	264	2 E69897	hypothetical prote
23	88.5	9.5	215	2 A84008	hemolysin III BH28
24	88.5	9.5	244	2 T22046	hypothetical prote
25	88	9.5	331	2 T23504	hypothetical prote
26	87	9.4	401	2 S42583	phosphate transloc
27	87	9.4	610	2 T32917	hypothetical prote
28	86.5	9.3	400	2 A41579	beta-3-adrenergic
29	86.5	9.3	400	2 A53281	beta 3-adrenergic

ALIGNMENTS

RESULT 1

A55046

plasmolipin - rat

C:Species: Rattus norvegicus (Norway rat)

C>Date: 18-Nov-1994 #sequence_revision 18-Nov-1994 #text_change 29-Sep-1999

C:Accession: A55046

R.Fischer, I.; Sapirstein, V.S.

J. Biol. Chem. 269, 24912-24919, 1994

A:Title: Molecular cloning of plasmolipin. Characterization of a novel proteolipid restr

A:Reference number: A55046; MUID:95014262; PMID:7929173

A:Accession: A55046

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-157 <FIS>

A:Cross-references: GB:U13617; NID:G532799; PIDN:AAA62133.1; PID:G532800

C:Superfamily: T-cell surface glycoprotein MAL

C:Keywords: lipoprotein; transmembrane protein

Query Match 79.7%; Score 741; DB 2; Length 157;

Best Local Similarity 87.9%; Pred. No. 3.6e-61;

Matches 138; Conservative 13; Mismatches 6; Indels 0; Gaps 0;

Qy	26	LRPDIGFVRSRLGALMLQLVLGLLWALIAADTPYHLYPAYGWVNFVAVFLWLTIVLFN	85
Db	1	MRPDLGFVRSALGVLLQLVLGLLWALIAADTPYHLYPAYGWVNFVAVFLWLTIVFFI	60
Qy	86	LYLQLHMKLYMPVLMIFNISATVYITATACSAVDLTSLRGTRFYNORAAASF	145
Db	61	TYLQLHMKLYMPVLLVFFVAAVLYITAFVACAAVDLTSLRGSRFYNORAAASF	120
Qy	146	FACLVMIAYGVSAFFSYQAWRGVGSNAATSQMAGGYA	182
Db	121	FACLVMIAYGLSAFFSFOAWRGVGSNAATSQMAGGYS	157

RESULT 2

T29464

hypothetical protein F28H1.4 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C:Accession: T29464

R.Du, Z.; Le, T.T.

A:Description: The sequence of C. elegans cosmid F28H1.

A:Reference number: Z20622

A:Accession: T29464

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-281 <DUZ>

A:Cross-references: UNIPROT:P83386; EMBL:U97013; PIDN:AAB52340.1; GSPDB:GN00019; CESP:F2

A:Experimental source: strain Bristol N2; clone F28H1

C:Genetics:

A:Gene: CESP:F28H1.4

A:Map position: 1

A:Introns: 4/1; 66/3; 108/3; 150/1; 188/3; 235/3

Query Match 17.0%; Score 158; DB 2; Length 281;

Best Local Similarity 28.6%; Pred. No. 2.7e-07;

Matches 50; Conservative 27; Mismatches 76; Indels 22; Gaps 5;

QY 18 GAEASVSALRDLGFRSRLGALMLQLVLGLLWVLIADTPYHLYPAYGWMVFAVFLW 77

DB 104 GPVRIEPPRLDCYIRTLGIMKIVICVLCILTFIFWMGPAY-YTCVGWATFVSUGI 162

QY 78 LVTIVLNLVLFQHLMKLVMPVPLVL-----MIFNISATVLYITAFIACSAV 126

DB 163 FVTSLLTLYLFRVVDLTPSLNNITVCLSTRTEIIIFQEMVVCFAWTVFPIA--ACVLAV 220

QY 127 DLTSIRGTRPNYQRAAASFFACLVMIAYGVSAFYSQARG-----VGSNAATSQ 176

DB 221 ASSQFRGTFAW---AIAAFAGACAYGDCYKLFUSKNERATGGSNPVVIQ 272

RESULT 3

A29472

T-cell surface glycoprotein MAL, splice form a - human

N:Alternate names: MAL proteolipid

C:Species: Homo sapiens (man)

C:Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 09-Jul-2004

C:Accession: A29472; S40076; S40077; S40079; S40078; A54680; I38009; S38933; S38934; S38

R:Alonso, M.A.; Weisman, S.M.

Proc. Natl. Acad. Sci. U.S.A. 84, 1997-2001, 1987

A:Title: cDNA cloning and sequence of MAL, a hydrophobic protein associated with human T

A:Reference number: A29472; MUID: 87175600; PMID: 3494249

A:Accession: A29472

A:Molecule type: DNA

A:Residues: 1-153 <ALO>

A:Cross-references: UNIPROT:P21145; GB:M15800; NID:G187297; PIDN:AAA36196.1; PID:G307157

R:Rancano, C.; Rubio, T.; Alonso, M.A.

submitted to the EMBL Data Library, December 1993

A:Description: Alternative splicing of human T-cell specific MAL mRNA and its correlatio

A:Reference number: S40076

A:Accession: S40076

A:Molecule type: mRNA

A:Residues: 1-153 <RAN>

A:Cross-references: EMBL:X76678; NID:G435477; PIDN:CAA54100.1; PID:G435478

A:Note: MAL-a

A:Accession: S40077

A:Molecule type: mRNA

A:Residues: 1-87,130-153 <RAW>

A:Cross-references: EMBL:X76679; NID:G435479; PIDN:CAA54101.1; PID:G435480

A:Note: MAL-b

A:Accession: S40079

A:Molecule type: mRNA

A:Residues: 1-31,130-153 <RAF>

A:Cross-references: EMBL:X76681; NID:G435481; PIDN:CAA54103.1; PID:G435482

A:Note: MAL-d

A:Accession: S40078

A:Molecule type: mRNA

A:Residues: 1-31,88-153 <RAA>

A:Cross-references: EMBL:X76680; NID:G435483; PIDN:CAA54102.1; PID:G435484

A:Note: MAL-c

R:Rancano, C.; Rubio, T.; Alonso, M.A.

Genomics 21, 447-450, 1994

A:Title: Alternative splicing of human T-cell-specific MAL mRNA and its correlation with

A:Reference number: A54680; MUID: 94375076; PMID: 8088843

A:Accession: A54680

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-153 <RA2>

A:Cross-references: GB:X76678; NID:G435477; PIDN:CAA54100.1; PID:G435478

R:Rancano, C.; Rubio, T.; Correas, I.; Alonso, M.A.

J. Biol. Chem. 269, 8159-8164, 1994

A:Title: Genomic structure and subcellular localization of MAL, a human T-cell-specific

A:Reference number: I38009; MUID: 94179150; PMID: 8132541

A:Accession: I38009

A>Status: Preliminary

A:Molecule type: DNA

A:Residues: 1-31 <RES>

A:Cross-references: EMBL:X76220; NID:G433225; PID:G1200084

A:Experimental source: Placenta

A:Note: submitted to the EMBL Data Library, November 1993

C:Genetics:

A:Gene: GDB:MAL

A:Cross-references: GDB:119374; OMIM:188860

A:Map position: 2cen-2q13

A:Introns: 31/3; 87/3; 129/3

C:Superfamily: T-cell surface glycoprotein MAL

C:Keywords: alternative splicing; endoplasmic reticulum; glycoprotein; T-cell; transmembr

F:1-153/Product: T-cell surface glycoprotein MAL, splice form a #status predicted <MAA>

F:1-87,130-153/Product: T-cell surface glycoprotein MAL, splice form b #status predicted

F:1-31,88-153/Product: T-cell surface glycoprotein MAL, splice form c #status predicted

F:1-31,130-153/Product: T-cell surface glycoprotein MAL, splice form d #status predicted

Query Match

Best Local Similarity 16.5%; Score 153; DB 2; Length 153;

Matches 45; Conservative 25; Mismatches 61; Indels 18; Gaps 6;

QY 22 SVSALRPDLGFRSRLGALMLQLVLGLLWVLIADT--PYHLYPAYGWMVFAVFLW 79

DB 17 SVFTTLPLD-----LFIPEFIFGLVWILVASSLVPWPL--VQGWVNFVSFQFVA 65

QY 80 TIVLNLVLFQHLMKLVMPVPLVIMIFNISATVLYITAFIACSAAVDLTSLRG--TRPY 137

DB 66 TTTLLIILYIGAAGG--ETSNVTLDAVAHCTAALFYLSASV-LEALATITMQDGFYRHY 122

QY 138 NORAAASFFACLVMIAYGVSAFYSQAWR 166

DB 123 HENIAAVVFSYIATLLYVYHVAVSLIRWK 151

RESULT 4

I38891

hypotheical protein - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 01-Nov-1996 #sequence_revision 01-Nov-1996 #text_change 09-Jul-2004

C:Accession: I38891

R:Lautner-Rieske, A.; Thiebe, R.; Zachau, H.G.

Gene 159, 159-202, 1995

A:Title: Searching for non-v kappa transcripts from the human immunoglobulin kappa locus

A:Reference number: I38891; MUID: 95347597; PMID: 7622049

A:Accession: I38891

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-148 <RBS>

A:Cross-references: UNIPROT:Q13021; EMBL:U17077; NID:G1000711; PIDN:AAA76738.1; PID:G1000

C:Genetics:

A:Gene: BENE

C:Superfamily: T-cell surface glycoprotein MAL

Query Match

Best Local Similarity 16.0%; Score 148.5; DB 2; Length 148;

Matches 38; Conservative 31; Mismatches 52; Indels 5; Gaps 4;

QY 39 ALMLQLVLGLLWVLIADTPTVHLYP-AYGWMVFAVFLMVLTVLNLVLFQHLMKLYM 97

DB 24 AFFPELIFGLVWVVAAT-HIVYPLQGWVWVYSLTSLFSLMFLSLYLFQFYKR--F 80

QY 98 VPVPLVIMIFNISATVLYIT-AFIACSAAVDLTSLRTRPNQRAAASFFACLVMIAYGV 156

DB 81 ESWRVLSLHGTTGLYNGAAVLQVHATIVSEKLDLPRIYYINSAASFPATLTYL 140

QY 157 SAFPYS 162

DB 141 HAFSIY 146

RESULT 5

DB 337 VLAAGH 342

RESULT 12
A98195
glutamate transport protein ECs4529 [imported] - Escherichia coli (strain O157:H7, subtype glutamate transport protein ECs4529) - Escherichia coli (strain O157:H7, subtype glutamate transport protein ECs4529)
C:Species: Escherichia coli
C>Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C:Accession: A98195
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G. Gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genomic islands from a patient with hemolytic uremic syndrome
A:Reference: PubMed:11258796
A:Accession: A98195
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-401 <HAY>
A:Cross-references: UNIPROT:Q8XD83; GB:BA000007; PIDN:BAE37952.1; PID:g13364004; GSPDB:G13364004
A:Experimental source: strain O157:H7, substrate RIMD 050952
C:Genetics:
A:Gene: ECs4529
C:Superfamily: sodium-glutamate symport carrier protein

Query Match 9.8%; Score 91.5; DB 2; Length 401;
Best Local Similarity 24.2%; Pred. No. 0.49;
Matches 45; Conservative 33; Mismatches 81; Indels 27; Gaps 6;

QY 1 MAEPFSKVSTRTSPPAQGAASVSLRPDLGFVRSRLG-----ALMLLQLVLGLLWALI 55
DB 179 VARVLVKHSTTPNGIPDDQEVPTAFKPDVGVRMTLSLVLIETIAICLTGVGIQAQLL 238
QY 56 ADTPYHLYPAYGMVFVAFLWLVTIIVLENLXLFQLHKLMVMVPWPVLVLMIFNISATVLY 115
DB 239 AGTAPEL-PFIVCVLFVGV-----ILNSGLSM--MGFYRVFERAVSVLGNSVLSLFL 287
QY 116 ITAFIACSAADVLTSLRGTRPYNQRAAASPFACLVMTAYGVSAFFSQAWRGVGSNAATS 175
DB 288 AVALLMGLK-LWELASL-----ALPMLAILVVQTIFMALYAIFVTTWRMMGNKYDA 336
QY 176 QMAGGY 181
DB 337 VLAAGH 342

RESULT 13
B86042
glutamate transport [imported] - Escherichia coli (strain O157:H7, subtype glutamate transport [imported])
C:Species: Escherichia coli
C>Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C:Accession: B86042
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew, L.L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimantanta, E.; Potamousis, K.; Apodaca, Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; PMID:21074935; PMID:11206551
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-401 <STO>
A:Cross-references: UNIPROT:Q8XD83; GB:AB005174; NID:g12518413; PIDN:AAG58798.1; GSPDB:G12518413
A:Experimental source: strain O157:H7, substrate EDL933
C:Genetics:
A:Gene: glts
C:Superfamily: sodium-glutamate symport carrier protein

Query Match 9.8%; Score 91.5; DB 2; Length 401;
Best Local Similarity 24.2%; Pred. No. 0.49;
Matches 45; Conservative 33; Mismatches 81; Indels 27; Gaps 6;

QY 1 MAEPFSKVSTRTSPPAQGAASVSLRPDLGFVRSRLG-----ALMLLQLVLGLLWALI 55
DB 179 VARVLVKHSTTPNGIPDDQEVPTAFKPDVGVRMTLSLVLIETIAICLTGVGIQAQLL 238

QY 56 ADTPPHLYPATGWTGAVFAVELWLVTIVLFNLVLFQJLHMKLYMPWPLVLMIFNISATVLY 111
Db 239 ACTAFAEL-PTFVCLVFGV-----ILSNGLSN---MGFYRFFERAVSVLGNVLSLFL 287
QY 116 IFAFIACSAADVLTSLRGTRPYNQRAAASFFACLVMIAYGVSAFFSYQAWRGVGSNAATS 175
Db 288 ANALMGLK-LWELASL-----ALPMLAILVQTIFFMALYAIFVTWRMMGKNYDAA 336
QY 176 QMAGGY 181
Db 337 VLAAGH 342

RESULT 14
T2328
Hypothetical protein K04G2.9 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T2328
R:Gardner, A.
Submitted to the EMBL Data Library, July 1996
A:Reference number: Z19727
A:Accession: T2328
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-208 <MIL>
A:Cross-references: UNIPROT:Q21228; EMBL:Z75712; PIDN:CAE00046.1; GSPDB:GN0001
A:Experimental source: clone K04G2
C:Genetics:
A:Gene: CRSP:K04G2.9
A:Map position: 1
A:Introns: 22/2; 57/3; 175/3

Query Match 9.8%; Score 91; DB 2; Length 208;
Best Local Similarity 24.6%; Pred. No. 0.3;
Matches 45; Conservative 30; Mismatches 76; Indels 32; Gaps 8

QY 8 VSTRSSPAQGAASVSAL---RDLGFVRSRLGALMLQLVLGLLWALIAIDTPVHLYP 64
Db 17 VTTTREKTKYKEHSVSCGHGPTDKNYCLGPLGLLRIAEIFLCVIVCLITSV-FGPGP 75
QY 65 AYGVWYF-----VAVELWLVTIVLFNLVLFQJLHMK-LYMWPLVLMIFNISATVLY 116
Db 76 FXG-ILFGQTILLTVASVAMLLTFITLIAYFTLHSLDFFQCWREADLLENVICAVLEI 134
QY 117 TAFIA-----CSAAVDLTS-----LRGTRPYNQRAAASFFACLVMIAYGVSAFF 160
Db 135 VLSIVAYVYSTGSWNNCN---DIGDGIHNGCRILYEWAFASFLTFILGIFYALTAF 191
QY 161 SYQ 163
Db 192 THK 194

RESULT 15
D81515
cell shape-determining protein MrdB CPl002 [imported] - Chlamydomonada pneumoniae
C:Species: Chlamydomonada pneumoniae, Chlamydia pneumoniae
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C:Accession: D81515
R:Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.,
C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.;
Nucleic Acids Res. 28, 1397-1406, 2000
A:Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae
A:Reference number: A81500; MUID:20150255; PMID:10684935
A:Accession: D81515
A:Status: preliminary
A:Molecule type: DNA
A:Cross-references: UNIPROT:G9K1T9; GB:AE002257; GB:AE002161; NID:g7189902; P
C:Genetics:

179 VARVI.VKHSTTPNGTPTDDOEVPPTAFKKPDDVGRMITSLVLIETIALIAICTVKGKIVAOLL 238

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OM protein - protein search, using sw model

Run on: December 1, 2004, 15:28:57 ; Search time 193 Seconds

(without alignments)
542,581 Million cell updates/sec

Title: US-09-602-597A-4

Perfect score: 930

Sequence: 1 MAEFPKSVTRTSPAQAE.....QAWRGVGSNAATSQWAGGYA 182

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 02.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	930	100.0	182	1 PL1P_HUMAN	Q9V342 homo sapien
2	851	91.5	182	1 PL1P_MOUSE	Q9ACU2 mus musculus
3	851	91.5	182	2 BAC27916	Bac27916 mus muscu
4	848	91.2	182	1 PL1P_RAT	P47987 rattus norv
5	323	34.7	170	2 Q6GPN9	Q6GPN9 xenopus lae
6	322	34.6	173	1 CLF8_HUMAN	Q81ZV2 homo sapien
7	316	34.0	173	1 CLF8_MOUSE	Q9CZ14 mus musculus
8	312	33.5	173	2 Q71B06	Q71B06 rattus norv
9	312	33.5	173	2 AAQ10889	Aaql0889 rattus no
10	179	19.2	174	2 Q6GNS0	Q6GNS0 xenopus lae
11	168	18.1	175	2 Q8B108	Q8B108 mus musculus
12	166.5	17.9	270	2 P83386	P83386 caenorhabdi
13	165	17.7	176	2 Q7TPB7	Q7TPB7 rattus norv
14	165	17.7	176	2 AAH62388	Aah62388 rattus no
15	162	17.4	176	1 MAL2_HUMAN	Q96912 homo sapien
16	162	17.4	176	2 Q6P1M4	Q6P1M4 homo sapien
17	162	17.4	176	2 AAH64992	Aah64992 homo sapi
18	161	17.3	159	2 Q6DER3	Q6DER3 xenopus tro
19	155	16.7	153	1 MAL_MOUSE	Q09198 mus musculus
20	155	16.7	153	2 BAB23430	Bab23430 mus muscu
21	153	16.5	153	1 MAL_HUMAN	P21145 homo sapien
22	152	16.3	153	1 MAL_RAT	Q64349 rattus norv
23	149.5	16.1	208	1 CLF4_MOUSE	Q8CJ61 mus musculus
24	148.5	16.0	153	1 BENE_HUMAN	Q13021 homo sapien
25	147.5	15.9	154	1 BENE_MOUSE	Q91X49 mus musculus
26	147.5	15.9	154	2 BAC37487	Bac37487 mus muscu
27	147.5	15.9	234	1 CLF4_HUMAN	Q81Z15 homo sapien
28	147	15.8	220	2 Q6ZMD9	Q6ZMD9 homo sapien
29	147	15.8	220	2 RAD18789	Rad18789 homo sapi
30	145.5	15.6	153	1 MAL_CANFA	Q82996 canis famil
31	144	15.5	159	2 Q6PBB5	Q6PBB5 xenopus lae

32	144	15.5	159	2 AAH59789	Aah59789 xenopus l
33	141	15.2	156	2 P83387	P83387 caenorhabdi
34	140	15.1	148	2 Q7TPB6	Q7TPB6 rattus norv
35	138.5	14.9	189	2 Q7PW02	Q7PW02 anopheles g
36	137.5	14.8	298	2 Q7Z507	Q7Z507 homo sapien
37	137.5	14.8	322	1 MYDM_HUMAN	Q96S97 homo sapien
38	137.5	14.8	322	2 BAC11513	Bac11513 homo sapi
39	137	14.7	177	2 Q9VZ71	Q9VZ71 drosophila
40	133	14.3	173	2 Q9B9K0	Q9B9K0 homo sapien
41	133	14.3	173	2 AAH62544	Aah62544 homo sapi
42	132.5	14.2	208	2 Q6DGM6	Q6DGM6 brachydanio
43	131	14.1	173	2 Q7TQC1	Q7TQC1 mus musculu
44	131	14.1	282	2 Q8BPS8	Q8BPS8 mus musculu
45	131	14.1	296	1 MYDM_MOUSE	Q35682 mus musculu

ALIGNMENTS

RESULT 1					
PL1P_HUMAN					
ID	PL1P_HUMAN	STANDARD;	PRT;	182 AA.	
AC	Q9V342;				
DT	16-OCT-2001 (Rel. 40, Created)				
DT	16-OCT-2001 (Rel. 40, Last sequence update)				
DT	05-JUL-2004 (Rel. 44, Last annotation update)				
DE	Plasmolipin.				
GN	Name=TM4SF11; Synonym=PMLP;				
OS	Homo sapiens (Human)				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OK	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Kidney;				
RA	Xie B., Durie R., Sapirstein V.S.;				
RT	"Molecular cloning of human plasmolipin cDNA";				
RL	Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Ovary;				
RX	MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;				
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,				
RA	Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,				
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,				
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,				
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,				
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,				
RA	Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,				
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,				
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,				
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,				
RA	Villaion D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,				
RA	Fahey J., Helton E., Kettman M., Madan A.C., Rodrigues S., Sanchez A.,				
RA	Whiting M., Madan A.C., Young A.C., Shevchenko Y., Bouffard G.G.,				
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,				
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,				
RA	Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,				
RA	Schmurch A., Schein J.F., Jones S.J.M., Marra M.A.,				
RT	"Generation and initial analysis of more than 15,000 full-length human				
RL	and mouse cDNA sequences";				
CC	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).				
CC	-!- FUNCTION: Appears to be involved in myelination. Could also				
CC	participate in ion transport events as addition of plasmolipin to				
CC	lipid bilayers induces the formation of ion channels, which are				
CC	voltage-dependent and K(+) selective (By similarity).				
CC	-!- SUBUNIT: Hexamer arranged as a trimer of two plasmolipin subunits				
CC	(By similarity).				
CC	-!- SUBCELLULAR LOCATION: Integral membrane protein.				
CC	-!- SIMILARITY: Belongs to the MAL family.				
CC	-----				
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CC	between the Swiss Institute of Bioinformatics and the EMBL outstation				

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 CC or send an email to license@isb-sib.ch).

DR EMBL; AF137386; AAD33060.1; -;
 DR EMBL; BC022760; AA02760.1; -;
 DR GenBank; HGNC:18553; TM4SF11.
 DR MIM; 600340; -;
 DR InterPro; IPR008253; Marvel.
 DR Pfam; PF01284; MARVEL; 1.
 KW Ion transport; Ionic channel; Transmembrane; Transport.
 FT DOMAIN 1 35
 FT TRANSMEM 36 56
 FT DOMAIN 57 68
 FT TRANSMEM 69 89
 FT DOMAIN 90 99
 FT TRANSMEM 100 120
 FT DOMAIN 121 141
 FT TRANSMEM 142 162
 FT DOMAIN 163 182
 SQ SEQUENCE 182 AA; 19986 MW; 6F09AA080E2F67E8 CRC64;

Query Match 100.0%; Score 930; DB 1; Length 182;
 Best Local Similarity 100.0%; Pred. No. 5.5e-70;
 Matches 182; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASEFPKSVTRTSSPAQGAASVSALRPDLGFRVSRGLGMLLQLVLGLVWALLADTPY 60
 DB 1 MASEFPKSVTRTSSPAQGAASVSALRPDLGFRVSRGLGMLLQLVLGLVWALLADTPY 60
 QY 61 HLYPAVGWVNFVAVFLWLTIVLFLNLYLFLQHLWKLWVPLVLMFNISATVLYITAPI 120
 DB 61 HLYPAVGWVNFVAVFLWLTIVLFLNLYLFLQHLWKLWVPLVLMFNISATVLYITAPI 120
 QY 121 ACSAAVDLTSLRTRPYNQRAAASFFACLVMIAYGVSAFFSQVQWGVGSNAATSQMAGG 180
 DB 121 ACSAAVDLTSLRTRPYNQRAAASFFACLVMIAYGVSAFFSQVQWGVGSNAATSQMAGG 180
 QY 181 YA 182
 DB 181 YA 182

RESULT 2
 ID PLIP MOUSE STANDARD; PRT; 182 AA.
 AC QSDC2;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Plasmolipin.
 GN Name=TM4sf11; Synonyms=Plmp, Plapi;
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RC SEQUENCE FROM N.A.
 RC STRAIN=129/SvevTACfBr; TISSUE=Spleen;
 RX MEDLINE=21564391; PubMed=11707781;
 RA Hamacher M., Pippirs U., Koehler A., Mueller H.W., Bosse F.;
 RT "Plasmolipin: genomic structure, chromosomal localization, protein
 RT expression pattern and putative association with Bardet-Biedl
 RT syndrome.";
 RL Mamm. Genome 12:933-937(2001).
 RN [2]

RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Kidney;
 RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 RA Nikaide I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,

RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
 RA Baldarelli R., Hill D.P., Buit C., Hume D.A., Quackenbush J.,
 RA Schirrell L.M., Kapran A., Matsuda H., Batalov S., Beisel K.W.,
 RA Blake J.A., Braggi T.A., Brusic V., Chothia C., Corbani L.E., Cousins S.,
 RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
 RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
 RA Kanai A., Kawai H., Kawasawa Y., Kedzierski R.M., King B.L.,
 RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
 RA Maglott D.R., Maltas L., Marchionni L., McKenzie L., Miki H.,
 RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramchandran S.,
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
 RA Sandelin A., Schneider C., Sempile C.A., Setou M., Shimada K.,
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
 RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
 RA Wilming L.G., Wyshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
 RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
 RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
 RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
 RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
 RA Birney E., Hayashizaki Y.;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 RN [3]

SEQUENCE FROM N.A.
 RP TISSUE=Colon;
 RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., McQuellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Mazny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Buttefield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903(2002).
 CC -!- FUNCTION: Appears to be involved in myelination. Could also
 CC participate in ion transport events as addition of plasmolipin to
 CC lipid bilayers induces the formation of ion channels, which are
 CC voltage-dependent and K(+) selective (By similarity).

CC -!- SUBUNIT: Hexamer arranged as a trimer of two plasmolipin subunits
 CC (By similarity).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: Belongs to the MAL family.

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 DR EMBL; AJ298129; CAC88126.1; -;
 DR EMBL; AJ298130; CAC88126.1; JOINED.
 DR EMBL; AK002477; BAB22130.1; -;
 DR EMBL; BC024534; AAH24534.1; -;
 DR MGI; MGI:1915051; Tm4sf11.

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DR InterPro: IPR008253; Marvel.
DR Pfam: PF01284; MARVEL; 1.
KW Ion transport; Ionic channel; Transmembrane; Transport.
FT DOMAIN 1 35 Cytoplasmic (Potential).
FT TRANSMEM 36 56 Extracellular (Potential).
FT DOMAIN 57 68 Extracellular (Potential).
FT TRANSMEM 69 89 Potent.
FT DOMAIN 90 99 Cytoplasmic (Potential).
FT TRANSMEM 100 120 Potent.
FT DOMAIN 121 141 Extracellular (Potential).
FT TRANSMEM 142 162 Potent.
FT DOMAIN 163 182 Cytoplasmic (Potential).
SQ SEQUENCE 182 AA; 19801 MW; F2D78E5E22173B42 CRC64;

Query Match 91.5%; Score 851; DB 1; Length 182;
Best Local Similarity 90.1%; Pred. No. 2.2e-63;
Matches 164; Conservative 9; Mismatches 9; Indels 0; Gaps 0;

QY 1 MAEPFSKVSTRTSSPAQGAASVSALRDLGFRSRLGALMLQLVGLLVWALIADTPY 60
DB 1 MAEPFSKVSTRTSSPAQGVASVSALRDLGFRSALGVALLQLGLLVWALIADTPY 60

QY 61 HLYPAYGWMFVAVFLWLVTVILENLYLFOLHMKLYMPWPLVLMIFNISATVLYITAFI 120
DB 61 HLYPAYGWMFVAVFLWLVTVIFFIYLFOLHMKLYMPWPLVLLIFFVAATVLYITAFI 120

QY 121 ACSAAVDLTSLRGTRPYNQRAAASFFACLVMIAYGVSAFFSYQAWRGVGSNAATSQWAGG 180
DB 121 ACAAAVDLTSLRGSRPYNQRAASFFACLVMIAYGVSAFFSFQAWRGVGSNAATSQWAGG 180

QY 181 YA 182
DB 181 YS 182

RESULT 3
BAC27916 PRELIMINARY; PRT; 182 AA.
ID BAC27916 PRELIMINARY; PRT; 182 AA.
AC BAC27916;
DT 14-APR-2004 (TREMELrel. 27, Created)
DT 14-APR-2004 (TREMELrel. 27, Last sequence update)
DT 14-APR-2004 (TREMELrel. 27, Last annotation update)
DE Adult male olfactory brain cDNA, RIKEN full-length enriched library,
DE clone:6430887D16 product:PLASMOLIPIN homolog.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Olfactory brain;
RX MEDLINE=22354683; PubMed=12466951;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Olfactory brain;
RX MEDLINE=21085660; PubMed=11217851;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Olfactory brain;
RX MEDLINE=99279253; PubMed=10349636;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [4]
RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Olfactory brain;
RX MEDLINE=20493374; PubMed=11042159;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Olfactory brain;
RX MEDLINE=20530913; PubMed=11076861;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Axiyama J., Nishi K., Kitsuami T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yanamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohata E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Olfactory brain;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayaehida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito K., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AK032540; BAC27916.1; -
SQ SEQUENCE 182 AA; 19801 MW; F2D78E5E22173B42 CRC64;

Query Match 91.5%; Score 851; DB 2; Length 182;
Best Local Similarity 90.1%; Pred. No. 2.2e-63;
Matches 164; Conservative 9; Mismatches 9; Indels 0; Gaps 0;

QY 1 MAEPFSKVSTRTSSPAQGAASVSALRDLGFRSRLGALMLQLVGLLVWALIADTPY 60
DB 1 MAEPFSKVSTRTSSPAQGVASVSALRDLGFRSALGVALLQLGLLVWALIADTPY 60

QY 61 HLYPAYGWMFVAVFLWLVTVILENLYLFOLHMKLYMPWPLVLMIFNISATVLYITAFI 120
DB 61 HLYPAYGWMFVAVFLWLVTVIFFIYLFOLHMKLYMPWPLVLLIFFVAATVLYITAFI 120

QY 121 ACSAAVDLTSLRGTRPYNQRAAASFFACLVMIAYGVSAFFSYQAWRGVGSNAATSQWAGG 180
DB 121 ACAAAVDLTSLRGSRPYNQRAASFFACLVMIAYGVSAFFSFQAWRGVGSNAATSQWAGG 180

QY 181 YA 182
DB 181 YS 182

RESULT 4
PILP RAT
ID PILP RAT STANDARD; PRT; 182 AA.
AC P47987;
DT 01-FEB-1996 (Rel. 33, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Plasmolipin.
GN Name=Tm4sf11; Synonyms=Pmlp;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
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QY 68 WWMFVAVFLWLVITVILFNLVLFOLHMKLVMPVPLVLMIFNISATVLYITAFIACSAAYD 127
 DB 70 WWMFVAVFYVWLSVFFLHLITRANTRITKVPWSLVGLCFNGSAFVLYLIAAWEASSVN 129
 QY 128 LTSLGTPYQNRRAASFFACLVMIAYGVSAFFSYQAWR 166
 DB 130 -KDVHQHYNYSWTASSPFAFIVTVCYALSTYFSQAWR 167

RESULT 6

CLF8 HUMAN
 ID CLF8 HUMAN STANDARD; PRT; 173 AA.
 AC Q81W02; Q81W01;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Chemokine-like factor super family member 8.
 GN Name=CKLFSF8;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
 RC TISSUE=tonsil;
 RX MEDLINE=22666620; PubMed=12782130; DOI=10.1016/S0888-7543(03)00095-8;
 RA Han W., Ding P., Xu M., Wang L., Rui M., Shi S., Liu Y., Zheng Y.,
 RA Chen Y., Yang T., Ma D.;
 RT "Identification of eight genes encoding chemokine-like factor
 RT superfamily members 1-8 (CKLFSF1-8) by in silico cloning and
 RT experimental validation.";
 RL Genomics 81:609-617(2003).
 [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Hippocampus;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klauener R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ussid T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- TISSUE SPECIFICITY: Highly expressed in liver and pancreas.
 CC -!- SIMILARITY: Belongs to the chemokine-like factor family.
 CC
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 CC
 CC EMBL: AF74370; AAC73034.1;
 CC EMBL: BC041390; AAH41390.1;
 CC GenBank: HGNC:19179; CKLFSF8.
 DR MIM: 607891; -.

DR InterPro; IPR008253; Marvel.
 DR Pfam; PF01284; MARVEL; 1.
 KW Chemotaxis; Cytokine; Transmembrane.
 FT TRANSMEM 40 60 Potential.
 FT TRANSMEM 70 90 Potential.
 FT TRANSMEM 105 125 Potential.
 FT TRANSMEM 147 167 Potential.
 FT CONFLICT 24 24 F -> S (in Ref. 2).
 FT CONFLICT 41 41 P -> H (in Ref. 2).
 FT CONFLICT 79 79 F -> S (in Ref. 2).
 SQ SEQUENCE 173 AA; 19632 MW; 311364373EAC6EE CRC64;
 Query Match 34.6%; Score 322; DB 1; Length 173;
 Best Local Similarity 43.8%; Pred. No. 3.2e-19;
 Matches 71; Conservative 29; Mismatches 54; Indels 8; Gaps 2;
 QY 8 VSTRSSPAQGAASVSALRPDLGFRVSRIGALMLQLVGLVWALIADTPVHLYPAYG 67
 DB 12 VTITASSFAENPFTSSSPAYDREFLTLPGFLIVAEIVLGLVLTLAGTEYFRVPAFG 71
 QY 68 WWMFVAVFLWLVITVILFNLVLFOLHMKLVMPVPLVLMIFNISATVLYITAFIACSAAYD 127
 DB 72 WWMFVAVFYVWLSVFFLHLITRANTRITKVPWSLVGLCFNGSAFVLYLIAAWEASSVN 126
 QY 128 LTSLGTPYQNRRAASFFACLVMIAYGVSAFFSYQAWR 166
 DB 127 ASSVSPERDSHNFSWAASSFFAFVLTICVAGNTYFSFIAMR 168

RESULT 7

CLF8 MOUSE
 ID CLF8 MOUSE STANDARD; PRT; 173 AA.
 AC Q9CZR4;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Chemokine-like factor super family member 8.
 GN Name=CKlfsf8;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Leukocyte;
 RA Ding P., Han W., Li T., Yang T., Shi S., Tan Y., Ma D.;
 RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
 [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Embryo;
 RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
 RA Yagi K., Tomaru Y., Hasegawa Y., Negami A., Schonbach C., Gojobori T.,
 RA Baldarelli R., Hill D.P., Sult C., Hume D.A., Quackenbush J.,
 RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
 RA Blake J.A., Bradt D., Brusci V., Chothia C., Corbani L.E., Cousins S.,
 RA Dalla E., Dragani T.A., Fletcher C.P., Forrest A., Frazer K.S.,
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
 RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
 RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
 RA Knapkova A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
 RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
 RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tonita M.,
 RA Verardo R., Wagner L., Walstedt C., Wang Y., Watanabe Y., Wells C.,
 RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
 RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
 RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
 RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,

DB 130 RKENATVNLDRMLGNVAATIPAFYTVTCGCGCTVLGFREWR 173

RESULT 10
Q6GNSO PRELIMINARY; PRT; 174 AA.

ID AC Q6GNSO;
DT 05-JUL-2004 (TREMELrel. 27, Created)
DT 05-JUL-2004 (TREMELrel. 27, Last sequence update)
DE Hypothetical protein.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xeropodinae; Xenopus.
OX NCBI_TaxID=8335;

RN RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner K.H., Schmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B.B., Bucow K.H., Shaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huliy S.W.,
RA Villalon D.K., Muzy D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalios D.E., Schnurch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=22341132; PubMed=12454917;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
initiative.";
RL Dev. Dyn. 225:384-391(2002).

RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Klein S., Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073433; AAH73433.1; -
DR InterPro; IPR008253; Marvel.
DR Pfam; PF01284; MARVEL; 1.
KW Hypothetical protein.
SQ SEQUENCE 174 AA; 18914 MW; 271P97ED7A5DECBC CRC64;

Query Match 19.2%; Score 179; DB 2; Length 174;
Best Local Similarity 29.3%; Pred. No. 2.8e-07;
Matches 48; Conservative 29; Mismatches 75; Indels 12; Gaps 3;

QY 14 SPAQAASVSALRP-DLGFSRSLGALLQLGLLVLLIADTPHYLPAYGVWVFV 72
Db :|::||::||::||::||::||::||::||::||::||::||:
QY 73 AVFLMIVTLFNLVLFQHLKLYVPPLVLMIFNISVTLYITAFIACSAAVDLTSL- 131
Db :|::||::||::||::||::||::||::||::||::||:
Db 71 SVTAFCSSLLLVLFTGL-VHMIOQNMFVPLAVHLTAPFYFGFAVLAEAAVTSLANLI 129
QY 132 -----RGTRFPYNQRARSAFFACLVMIAYGSVAFFSVQAWR 166
Db :|::||::||::||::||::||::||::||::||::||:

SQ SEQUENCE 270 AA; 30171 MW; A163D751429C3E72 CRC64;
 Query Match 17.9%; Score 166.5; DB 2; Length 270;
 Best Local Similarity 29.9%; Pred. No. 4.5e-06;
 Matches 49; Conservative 27; Mismatches 77; Indels 11; Gaps 4;

QY	18	GAEASVSALRPDLGFVSRICGALMLLOLVLLGVWLIADTPHYLPAYGWTFVAVFLM	77
DB	104	GEAIVIEFPRDCDEIIRTLGGIKVICVLCLLTFTFVMWGPAI--YTGVGWATPVSSVGI	162
QY	78	LTVILFNLYLFQLHMKLNVVPPLVLMIFENISATVLYITAFIAGSAAVDLTSLRGTRPY	137
DB	163	FVTLSLLTLYLFRVVDLPSPINMTVCVMVCFANTVFFPIA--ACVLAVASSQPRGTFAW	220
QY	138	NORAAASFACLVMIAYGVSAFPSYQAWRG-----VGSNAATSQ	176
DB	221	---ATAAPFAFGAMCAYGFCYLKFLSKGNERATGSGNPVVIQ	261

RESULT 13
Q7TPB7
 ID Q7TPB7 PRELIMINARY; PRT; 176 AA.
 AC Q7TPB7;
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE MAL2A (Hypothetical protein).
 GN Name=Mal2a;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 ON NCBI TaxID=10116;
 RX [1]_TaxID=10116;
 RP SEQUENCE FROM N.A.
 RC STRAIN=NEDH; TISSUE=Pancreas;
 RA Gould F.K., Shennan K.I.J.;
 RL Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Prostate;
 RX MEDLINE=22389257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler N.K.,
 RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh X.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiruki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullighy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whirling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smalley D.E., Schnurch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Prostate;
 RA Strausberg R.;
 RL Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AY079080; AAL86010.1; -;
 DR EMBL; BC062388; AAH62388.1; -;
 DR GO; GO:0016020; C:membrane; IEA.
 DR InterPro; IPR008253; Marvel.
 DR Pfam; PF01284; MARVEL; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 176 AA; 19195 MW; B4A040D96FB68A45 CRC64;

Db	87	LSGWVTQI-DANNWFDPAYHFVVFYFGAFLEAAATSLHDLQCNNTWVVKPLNDNQ	145
Qy	137	YNORAAASFACLVMIATYGVSAFFSQAMR	166
Db	146	YNINVAATVFAFMTTACTYGCGLCLALRRWR	175
RESULT 15			
Mal2_HUMAN	STANDARD;	PRT;	176 AA.
AC	Q969L2;		
DT	28-FEB-2003 (Rel. 41, Created)		
DT	28-FEB-2003 (Rel. 41, Last sequence update)		
DT	05-JUL-2004 (Rel. 44, Last annotation update)		
DE	MAL2 protein.		
GN	Name=MAL2;		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A., TISSUE SPECIFICITY, AND INTERACTION WITH TPDS2L2.		
RX	MEDLINE=2143826; PubMed=11549320; DOI=10.1106/geno.2001.6610;		
RA	Wilson S.H.D., Bailey A.M., Nourse C.R., Mattei M.-G., Byrne J.A.;		
RT	"Identification of MAL2, a novel member of the mal proteolipid family,		
RT	though interactions with TPDS2-like proteins in the yeast two-hybrid		
RL	system";		
RL	Genomics 76:81-88(2001).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Ovary;		
RC	MEDLINE=223388257; PubMed=12477932; DOI=10.1073/pnas.242603899;		
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Dege J.G.,		
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,		
RA	Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,		
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,		
RA	Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,		
RA	Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,		
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,		
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,		
RA	Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,		
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,		
RA	Villalón D.K., Murry D.M., Sodergren E.J., Lu X., Gibbs R.A.,		
RA	Fahney J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,		
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,		
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,		
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,		
RA	Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,		
RA	Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;		
RT	"Generation and initial analysis of more than 15,000 full-length human		
RL	rat and mouse cDNA sequences.";		
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).		
CC	-1- SUBUNIT: Interacts with TPDS2L2.		
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).		
CC	-1- TISSUE SPECIFICITY: Predominantly expressed in kidney, lung, and		
CC	liver.		
CC	-1- SIMILARITY: Belongs to the MAL family.		
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration		
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announcement		
CC	or send an email to license@isb-sib.ch).		
DR	EMBL; AY007723; AAG15576.1; -		
DR	ENBL; BC012367; AAH12367.1; -		
DR	Genew; HGNC:13634; MAL2.		
DR	InterPro; IPR008253; Marvel.		
DR	Pfam; PF01284; MARVEL; 1.		
KT	Transmembrane.		
FT	TRANSMEM 35 55 Potential.		

```

FT      TRANSMEM      67      87      Potential.
FT      TRANSMEM      103     123      Potential.
FT      TRANSMEM      150     170      Potential.
SQ      SEQUENCE      176 AA; 19125 MW;  BACDA0BF3A26FD44  CRC64;

Query Match      17.4%;      Score 162;      DB 1;      Length 176;
Best Local Similarity 28.7%;      Pred. NO. 7.4e-06;
Matches 43;      Conservative 30;      Mismatches 63;      Indels 14;      Gaps 4;

Qy      28      PDLGPFVRSRGLMMLLOLVGLLWVLIADTPTVHLYPAGWVWVAVELWLVIVLENLY 87
      ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db      29      PDI - - LRTYSGAFVCLBELGGLVWLIVASSNVPELLQGWVWFVSTAFFSLLGLGMF 86

Qy      88      LFQLHMKLYWVPELVLUMINISATVLYYTATACSAVDL - - - - - TSLRG - - - - - TRP 136
      ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db      87      LSGWVAQI - DANNFLDFATVFFVYFGAFLEERAATSLHDLHCNTITITGQPELSDNQ 145

Qy      137      YNQRAAASFACLVMIAYGSVAFSQAWR 166
      ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db      146      YNINVAASIIFAFMTTACYGCSGLALRRWR 175

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Job time : 195 secs